

(19) World Intellectual Property Organization
International Bureau(43) International Publication Date
30 January 2003 (30.01.2003)

PCT

(10) International Publication Number
WO 03/008440 A2(51) International Patent Classification⁷: C07K 14/00

(21) International Application Number: PCT/EP02/07929

(22) International Filing Date: 16 July 2002 (16.07.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/305,806 16 July 2001 (16.07.2001) US
60/358,416 20 February 2002 (20.02.2002) US

(71) Applicant (for all designated States except US): SYNGENTA PARTICIPATIONS AG [CH/CH]; Schwarzwaldallee 215, CH-4058 Basel (CH).

(72) Inventors; and

(75) Inventors/Applicants (for US only): LEVIN, Joshua, Zvi [US/US]; Syngenta Biotechnology, Inc., 3054 Cornwallis Road, Research Triangle Park, NC 27709 (US). PATTON, David, Andrew [US/CH]; Syngenta Crop Protection AG, Werk Stein, Schaffhauserstrasse, CH-4332 Stein (CH). MCELVER, John, Alan [US/US]; Syngenta Biotechnology, Inc., 3054 Cornwallis Road, Research Triangle Park, NC 27709 (US). BUDZISZEWSKI, Gregory, Joseph [US/US]; Syngenta Biotechnology, Inc., 3054 Cornwallis Road, Research Triangle Park, NC 27709 (US). ZHOU, Qing [CN/US]; Syngenta Biotechnology, Inc., 3054 Cornwallis Road, Research Triangle Park, NC 27709 (US). AUX, George, W. [US/US]; Syngenta Biotechnology, Inc., 3054 Cornwallis Road, Research Triangle Park, NC 27709 (US). TOSSBERG, John [US/US]; Syngenta Biotechnology, Inc., 3054 Cornwallis Road, Research Triangle Park, NC 27709 (US). WEGRICH GLOVER, Lyn [US/US]; 5446 Escovet Lane, San Jose, CA 95118 (US). ASHBY, Carl, Sandidge [US/US]; Capital One FSD, 12061-0148, 11013 W. Broad Street, Glen Allen, VA 23060 (US). THOMAS, Carl, Randall [US/US];

Syngenta Biotechnology, Inc., 3054 Cornwallis Road, Research Triangle Park, NC 27709 (US). MADHAVEN, Ernie [US/US]; Falmouth, VA (US). LEWIS, Sharon [US/US]; Syngenta Biotechnology, Inc., 3054 Cornwallis Road, Research Triangle Park, NC 27709 (US). DUNN, Jill [US/US]; Syngenta Biotechnology, Inc., 3054 Cornwallis Road, Research Triangle Park, NC 27709 (US). CATES, Eddie [US/US]; Syngenta Biotechnology, Inc., 3054 Cornwallis Road, Research Triangle Park, NC 27709 (US). LAW, Marcus, Dixon [US/US]; Syngenta Biotechnology, Inc., 3054 Cornwallis Road, Research Triangle Park, NC 27709 (US).

(74) Agent: BASTIAN, Werner; Syngenta Participations AG, Intellectual Property, P.O. Box, CH-4002 Basel (CH).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

A2

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03/008440

(54) Title: NUCLEIC ACID MOLECULES ENCODING PROTEINS ESSENTIAL FOR PLANT GROWTH AND DEVELOPMENT AND USES THEREOF

(57) Abstract: Nucleotide sequences are isolated from *Arabidopsis thaliana* that code for proteins essential for plant growth and development. The essentially of the proteins may be exploited by recombinantly expressing the proteins and using them in screening assays to identify compounds that interact with or inhibit the proteins and are therefore potential herbicides.

**NUCLEIC ACID MOLECULES ENCODING PROTEINS ESSENTIAL FOR PLANT
GROWTH AND DEVELOPMENT AND USES THEREOF**

The present invention pertains to nucleic acid molecules isolated from *Arabidopsis thaliana* comprising nucleotide sequences that encode proteins essential for plant growth and development. The invention particularly relates to methods of using these proteins as herbicide targets, based on this essentiality.

The use of herbicides to control undesirable vegetation such as weeds in crop fields has become almost a universal practice. The herbicide market exceeds 15 billion dollars annually. Despite this extensive use, weed control remains a significant and costly problem for farmers.

Effective use of herbicides requires sound management. For instance, the time and method of application and stage of weed plant development are critical to achieving good weed control with herbicides. Because various weed species are resistant to herbicides, the production of effective new herbicides becomes increasingly important. New herbicides can now be discovered using high-throughput screens that implement recombinant DNA technology. Metabolic enzymes found to be essential to plant growth and development can be recombinantly produced through standard molecular biological techniques and utilized as herbicide targets in screens for novel inhibitors of the enzyme activity. More generally, any essential plant protein can be used to screen for inhibitors of its activity. The novel inhibitors discovered through such screens may then be used as herbicides to control undesirable vegetation.

In view of the above, there remain persistent and ongoing problems with unwanted or detrimental vegetation growth (e.g. weeds). Furthermore, as the population continues to grow, there will be increasing food shortages. Therefore, there exists a long felt, yet unfulfilled need, to find new, effective, and economic herbicides.

In view of these needs, it is an object of the invention to provide nucleic acid molecules from *Arabidopsis thaliana* comprising nucleotide sequences that encode proteins essential for plant growth and development. It is another object to provide the essential proteins encoded by these essential nucleotide sequences for assay development to identify

inhibitory compounds with herbicidal activity. It is still another object of the present invention to provide an effective and beneficial method for identifying new or improved herbicides using the essential proteins of the invention.

In furtherance of these and other objects, the present invention provides nucleic acid molecules isolated from *Arabidopsis thaliana* comprising nucleotide sequences that encode proteins essential for plant viability. Genetic results show that when any of the nucleotide sequences of the invention are mutated in *Arabidopsis thaliana*, the resulting phenotype is embryo or seedling lethal in the homozygous state. In particular, by using *Ac/Ds* transposon or T-DNA-mediated mutagenesis, the inventors of the present invention are the first to demonstrate that the activity of each protein of the present invention is essential for plant growth in *Arabidopsis thaliana*.

This knowledge is exploited to provide novel herbicide modes of action. The critical role in plant growth of the proteins encoded by each of the nucleotide sequences of the invention implies that chemicals that inhibit the function of any one of these proteins in plants are likely to have detrimental effects on plants and are potentially good herbicide candidates. Thus, the proteins encoded by the essential nucleotide sequences provide the bases for assays designed to easily and rapidly identify novel herbicides.

The present invention therefore provides methods of using a purified protein encoded by any one of the nucleotide sequences described below to identify inhibitors thereof, which can then be used as herbicides to suppress the growth of undesirable vegetation, *e.g.* in fields where crops are grown, particularly agronomically important crops such as maize and other cereal crops such as wheat, oats, rye, sorghum, rice, barley, millet, turf and forage grasses, and the like, as well as cotton, sugar cane, sugar beet, oilseed rape, and soybeans.

Disclosed herein are nucleic acid molecules isolated from *Arabidopsis thaliana*. In one embodiment, the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence, the complement of which hybridizes under stringent conditions to a sequence selected from the group consisting of the odd numbered SEQ ID NOs:1-95. In another embodiment, the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a protein comprising an amino acid sequence having at least 60%, preferably 70%, more preferably 80%, still more preferably 90%, even more preferably 95%, and most preferably 99-100% sequence identity to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.

The present invention also provides a chimeric construct comprising a promoter operatively linked to a nucleic acid molecule according to the present invention, wherein the promoter is preferably functional in a eukaryote, wherein the promoter is preferably heterologous to the nucleic acid molecule. The present invention further provides a 5 recombinant vector comprising a chimeric construct according to the present invention, wherein said vector is capable of being stably transformed into a host cell. The present invention still further provides a host cell comprising a nucleic acid molecule according to the present invention, wherein said nucleic acid molecule is preferably expressible in the cell. The host cell is preferably selected from the group consisting of a plant cell, a yeast cell, an 10 insect cell, and a prokaryotic cell. The present invention additionally provides a plant or seed comprising a plant cell according to the present invention.

The present invention also provides proteins essential for plant growth in *Arabidopsis thaliana*. In one embodiment, the present invention provides an isolated protein comprising an amino acid sequence having at least 60%, preferably 70%, more preferably 80%, still more 15 preferably 90%, even more preferably 95%, and most preferably 99-100% sequence identity to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. In accordance with another embodiment, the present invention also relates to the recombinant production of proteins of the invention and methods of using the proteins of the invention in assays for identifying compounds that interact with the protein.

According to another aspect, the present invention provides a method of identifying a 20 herbicidal compound, comprising: (a) combining a polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96 with a compound to be tested for the ability to bind to said polypeptide, under conditions conducive to binding; (b) selecting a compound 25 identified in (a) that binds to said polypeptide; (c) applying a compound selected in (b) to a plant to test for herbicidal activity; and (d) selecting a compound identified in (c) that has herbicidal activity. Preferably, the polypeptide comprises an amino acid sequence at least 95% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. More preferably, the polypeptide comprises an amino acid 30 sequence at least 99% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. Most preferably, the polypeptide comprises an amino acid sequence selected from the group consisting of the even numbered SEQ ID

NOs:2-96. The present invention also provides a method for killing or inhibiting the growth or viability of a plant, comprising applying to the plant a herbicidal compound identified according to this method.

According to yet another aspect, the present invention provides a method of
5 identifying a herbicidal compound, comprising: (a) combining a polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96 with a compound to be tested for the ability to inhibit the activity of said polypeptide, under conditions conducive to inhibition; (b) selecting a compound identified in (a) that inhibits the activity of said polypeptide; (c)
10 applying a compound selected in (b) to a plant to test for herbicidal activity; and (d) selecting a compound identified in (c) that has herbicidal activity. Preferably, the polypeptide comprises an amino acid sequence at least 95% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. More preferably, the polypeptide comprises an amino acid sequence at least 99% identical to an amino acid
15 sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. Most preferably, the polypeptide comprises an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. The present invention also provides a method for killing or inhibiting the growth or viability of a plant, comprising applying to the plant a herbicidal compound identified according to this method.

20 The present invention still further provides a method for killing or inhibiting the growth or viability of a plant, comprising inhibiting expression in said plant of a protein having at least 60%, preferably 70%, more preferably 80%, still more preferably 90%, even more preferably 95%, and most preferably 99-100% sequence identity to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.

25 Other objects and advantages of the present invention will become apparent to those skilled in the art and from a study of the following description of the invention and non-limiting examples. The entire contents of all publications mentioned herein are hereby incorporated by reference.

30 BRIEF DESCRIPTION OF THE SEQUENCES IN THE SEQUENCE LISTING

Odd numbered SEQ ID NOs:1-95 are nucleotide sequences isolated from *Arabidopsis thaliana* that are more fully described in Table 5 below.

Even numbered SEQ ID NOs:2-96 are protein sequences encoded by the immediately preceding nucleotide sequence, *e.g.*, SEQ ID NO:2 is the protein encoded by the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:4 is the protein encoded by the nucleotide sequence of SEQ ID NO:3, etc.

5 SEQ ID NOs:101-125 are PCR primers.

DEFINITIONS

For clarity, certain terms used in the specification are defined and presented as follows:

10 “Associated with / operatively linked” refer to two nucleic acid sequences that are related physically or functionally. For example, a promoter or regulatory DNA sequence is said to be “associated with” a DNA sequence that codes for an RNA or a protein if the two sequences are operatively linked, or situated such that the regulator DNA sequence will affect the expression level of the coding or structural DNA sequence.

15 A “chimeric construct” is a recombinant nucleic acid sequence in which a promoter or regulatory nucleic acid sequence is operatively linked to, or associated with, a nucleic acid sequence that codes for an mRNA or which is expressed as a protein, such that the regulatory nucleic acid sequence is able to regulate transcription or expression of the associated nucleic acid sequence. The regulatory nucleic acid sequence of the chimeric construct is not normally 20 operatively linked to the associated nucleic acid sequence as found in nature.

25 Co-factor: natural reactant, such as an organic molecule or a metal ion, required in an enzyme-catalyzed reaction. A co-factor is *e.g.* NAD(P), riboflavin (including FAD and FMN), folate, molybdopterin, thiamin, biotin, lipoic acid, pantothenic acid and coenzyme A, S-adenosylmethionine, pyridoxal phosphate, ubiquinone, menaquinone. Optionally, a co-factor can be regenerated and reused.

A “coding sequence” is a nucleic acid sequence that is transcribed into RNA such as mRNA, rRNA, tRNA, snRNA, sense RNA or antisense RNA. Preferably the RNA is then translated in an organism to produce a protein.

30 Complementary: “complementary” refers to two nucleotide sequences that comprise antiparallel nucleotide sequences capable of pairing with one another upon formation of hydrogen bonds between the complementary base residues in the antiparallel nucleotide sequences.

Enzyme activity: means herein the ability of an enzyme to catalyze the conversion of a substrate into a product. A substrate for the enzyme comprises the natural substrate of the enzyme but also comprises analogues of the natural substrate, which can also be converted, by the enzyme into a product or into an analogue of a product. The activity of the enzyme is measured for example by determining the amount of product in the reaction after a certain period of time, or by determining the amount of substrate remaining in the reaction mixture after a certain period of time. The activity of the enzyme is also measured by determining the amount of an unused co-factor of the reaction remaining in the reaction mixture after a certain period of time or by determining the amount of used co-factor in the reaction mixture after a certain period of time. The activity of the enzyme is also measured by determining the amount of a donor of free energy or energy-rich molecule (e.g. ATP, phosphoenolpyruvate, acetyl phosphate or phosphocreatine) remaining in the reaction mixture after a certain period of time or by determining the amount of a used donor of free energy or energy-rich molecule (e.g. ADP, pyruvate, acetate or creatine) in the reaction mixture after a certain period of time.

Essential: an “essential” *Arabidopsis thaliana* nucleotide sequence is a nucleotide sequence encoding a protein such as e.g. a biosynthetic enzyme, receptor, signal transduction protein, structural gene product, or transport protein that is essential to the growth or survival of the plant.

Expression Cassette: “Expression cassette” as used herein means a nucleic acid molecule capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operatively linked to the nucleotide sequence of interest which is operatively linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The coding region usually codes for a protein of interest but may also code for a functional RNA of interest, for example antisense RNA or a nontranslated RNA, in the sense or antisense direction. The expression cassette comprising the nucleotide sequence of interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one that is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. Typically, however, the expression cassette is heterologous with respect to the host, i.e., the particular DNA sequence of the expression cassette does not occur naturally in the host cell and must have been introduced into the host cell or an ancestor of the host cell by a transformation event. The expression of

the nucleotide sequence in the expression cassette may be under the control of a constitutive promoter or of an inducible promoter that initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a multicellular organism, such as a plant, the promoter can also be specific to a particular tissue or organ or stage of 5 development.

Gene: the term "gene" is used broadly to refer to any segment of DNA associated with a biological function. Thus, genes include coding sequences and/or the regulatory sequences required for their expression. Genes also include nonexpressed DNA segments that, for example, form recognition sequences for other proteins. Genes can be obtained from a variety 10 of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

Heterologous/exogenous: The terms "heterologous" and "exogenous" when used herein to refer to a nucleic acid sequence (e.g. a DNA sequence) or a gene, refer to a sequence 15 that originates from a source foreign to the particular host cell or, if from the same source, is modified from its original form. Thus, a heterologous gene in a host cell includes a gene that is endogenous to the particular host cell but has been modified through, for example, the use of DNA shuffling. The terms also include non-naturally occurring multiple copies of a naturally occurring DNA sequence. Thus, the terms refer to a DNA segment that is foreign or 20 heterologous to the cell, or homologous to the cell but in a position within the host cell nucleic acid in which the element is not ordinarily found. Exogenous DNA segments are expressed to yield exogenous polypeptides.

A "homologous" nucleic acid (e.g. DNA) sequence is a nucleic acid (e.g. DNA) sequence naturally associated with a host cell into which it is introduced.

25 Hybridization: The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA. "Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be 30 accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target nucleic acid sequence.

5 Inhibitor: a chemical substance that inactivates the enzymatic activity of a protein such as a biosynthetic enzyme, receptor, signal transduction protein, structural gene product, or transport protein. The term "herbicide" (or "herbicidal compound") is used herein to define an inhibitor applied to a plant at any stage of development, whereby the herbicide inhibits the growth of the plant or kills the plant.

Interaction: quality or state of mutual action such that the effectiveness or toxicity of one protein or compound on another protein is inhibitory (antagonists) or enhancing (agonists).

10 A nucleic acid sequence is "isocoding with" a reference nucleic acid sequence when the nucleic acid sequence encodes a polypeptide having the same amino acid sequence as the polypeptide encoded by the reference nucleic acid sequence.

Isogenic: plants that are genetically identical, except that they may differ by the presence or absence of a heterologous DNA sequence.

15 Isolated: in the context of the present invention, an isolated DNA molecule or an isolated enzyme is a DNA molecule or enzyme that, by the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated DNA molecule or enzyme may exist in a purified form or may exist in a non-native environment such as, for example, in a transgenic host cell.

20 Mature protein: protein from which the transit peptide, signal peptide, and/or propeptide portions have been removed.

Minimal Promoter: the smallest piece of a promoter, such as a TATA element, that can support any transcription. A minimal promoter typically has greatly reduced promoter activity in the absence of upstream activation. In the presence of a suitable transcription factor, the minimal promoter functions to permit transcription.

25 Modified Enzyme Activity: enzyme activity different from that which naturally occurs in a plant (*i.e.* enzyme activity that occurs naturally in the absence of direct or indirect manipulation of such activity by man), which is tolerant to inhibitors that inhibit the naturally occurring enzyme activity.

Native: refers to a gene that is present in the genome of an untransformed plant cell.

30 Naturally occurring: the term "naturally occurring" is used to describe an object that can be found in nature as distinct from being artificially produced by man. For example, a protein or nucleotide sequence present in an organism (including a virus), which can be

isolated from a source in nature and which has not been intentionally modified by man in the laboratory, is naturally occurring.

Nucleic acid: the term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form. Unless specifically limited, 5 the term encompasses nucleic acids containing known analogues of natural nucleotides which have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g. degenerate codon substitutions) and complementary sequences and as well as the sequence 10 explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer *et al.*, *Nucleic Acid Res.* 19: 5081 (1991); Ohtsuka *et al.*, *J. Biol. Chem.* 260: 2605-2608 (1985); Rossolini *et al.*, *Mol. Cell. Probes* 8: 91-98 (1994)). The terms "nucleic acid" or "nucleic acid sequence" may also 15 be used interchangeably with gene, cDNA, and mRNA encoded by a gene.

"ORF" means open reading frame.

Percent identity: the phrases "percent identical" or "percent identical," in the context of two nucleic acid or protein sequences, refers to two or more sequences or subsequences that have for example 60%, preferably 70%, more preferably 80%, still more preferably 90%, 20 even more preferably 95%, and most preferably at least 99% nucleotide or amino acid residue identity, when compared and aligned for maximum correspondence, as measured using one of the following sequence comparison algorithms or by visual inspection. Preferably, the percent identity exists over a region of the sequences that is at least about 50 residues in length, more preferably over a region of at least about 100 residues, and most preferably the 25 percent identity exists over at least about 150 residues. In an especially preferred embodiment, the percent identity exists over the entire length of the coding regions.

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2: 482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48: 443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85: 2444 (1988), by 5 computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by visual inspection (*see generally*, Ausubel *et al.*, *infra*).

One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al.*, *J. Mol. Biol.* 215: 403-410 (1990). Software for performing BLAST analyses is publicly available 10 through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some 15 positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, 1990). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for 20 as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due 25 to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults 30 a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89: 10915 (1989)).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see, e.g.*, Karlin &

Altschul, *Proc. Nat'l. Acad. Sci. USA* 90: 5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered 5 similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

Pre-protein: protein that is normally targeted to a cellular organelle, such as a chloroplast, and still comprises its native transit peptide.

10 Purified: the term "purified," when applied to a nucleic acid or protein, denotes that the nucleic acid or protein is essentially free of other cellular components with which it is associated in the natural state. It is preferably in a homogeneous state although it can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high 15 performance liquid chromatography. A protein that is the predominant species present in a preparation is substantially purified. The term "purified" denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Particularly, it means that the nucleic acid or protein is at least about 50% pure, more preferably at least about 85% pure, and most preferably at least about 99% pure.

20 Two nucleic acids are "recombined" when sequences from each of the two nucleic acids are combined in a progeny nucleic acid. Two sequences are "directly" recombined when both of the nucleic acids are substrates for recombination. Two sequences are "indirectly recombined" when the sequences are recombined using an intermediate such as a cross-over oligonucleotide. For indirect recombination, no more than one of the sequences is an actual 25 substrate for recombination, and in some cases, neither sequence is a substrate for recombination.

30 "Regulatory elements" refer to sequences involved in controlling the expression of a nucleotide sequence. Regulatory elements comprise a promoter operatively linked to the nucleotide sequence of interest and termination signals. They also typically encompass sequences required for proper translation of the nucleotide sequence.

Significant Increase: an increase in enzymatic activity that is larger than the margin of error inherent in the measurement technique, preferably an increase by about 2-fold or greater

of the activity of the wild-type enzyme in the presence of the inhibitor, more preferably an increase by about 5-fold or greater, and most preferably an increase by about 10-fold or greater.

5 Significantly less: means that the amount of a product of an enzymatic reaction is reduced by more than the margin of error inherent in the measurement technique, preferably a decrease by about 2-fold or greater of the activity of the wild-type enzyme in the absence of the inhibitor, more preferably an decrease by about 5-fold or greater, and most preferably an decrease by about 10-fold or greater.

Specific Binding/Immunological Cross-Reactivity: An indication that two nucleic acid sequences or proteins are substantially identical is that the protein encoded by the first nucleic acid is immunologically cross reactive with, or specifically binds to, the protein encoded by the second nucleic acid. Thus, a protein is typically substantially identical to a second protein, for example, where the two proteins differ only by conservative substitutions. The phrase "specifically (or selectively) binds to an antibody," or "specifically (or selectively) immunoreactive with," when referring to a protein or peptide, refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions 10 may require an antibody that is selected for its specificity for a particular protein. For example, antibodies raised to the protein with the amino acid sequence encoded by any of the nucleic acid sequences of the invention can be selected to obtain antibodies specifically immunoreactive with that protein and not with other proteins except for polymorphic variants. A variety of immunoassay formats may be used to select antibodies specifically 15 immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays, Western blots, or immunohistochemistry are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) *Antibodies, A Laboratory Manual*, Cold Spring Harbor Publications, New York ("Harlow and Lane"), for a description of immunoassay formats and conditions that can be used to determine specific 20 immunoreactivity. Typically a specific or selective reaction will be at least twice background signal or noise and more typically more than 10 to 100 times background.

"Stringent hybridization conditions" and "stringent hybridization wash conditions" in the context of nucleic acid hybridization experiments such as Southern and Northern hybridizations are sequence dependent, and are different under different environmental parameters. Longer sequences hybridize specifically at higher temperatures. An extensive 5 guide to the hybridization of nucleic acids is found in Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology-Hybridization with Nucleic Acid Probes* part I chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays" Elsevier, New York. Generally, highly stringent hybridization and wash conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at 10 a defined ionic strength and pH. Typically, under "stringent conditions" a probe will hybridize to its target subsequence, but to no other sequences.

The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Very stringent conditions are selected to be equal to the T_m for a particular probe. An example of stringent hybridization 15 conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern blot is 50% formamide with 1 mg of heparin at 42°C, with the hybridization being carried out overnight. An example of highly stringent wash conditions is 0.1 5M NaCl at 72°C for about 15 minutes. An example of stringent wash conditions is a 0.2x SSC wash at 65°C for 15 minutes (see, Sambrook, *infra*, 20 for a description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, *e.g.*, more than 100 nucleotides, is 1x SSC at 45°C for 15 minutes. An example low stringency wash for a duplex of, *e.g.*, more than 100 nucleotides, is 4-6x SSC at 25 40°C for 15 minutes. For short probes (*e.g.*, about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1.0 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is typically at least about 30°C. Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2x (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a 30 specific hybridization. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the proteins that they encode are substantially

identical. This occurs, *e.g.*, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

The following are examples of sets of hybridization/wash conditions that may be used to clone nucleotide sequences that are homologues of reference nucleotide sequences of the present invention: a reference nucleotide sequence preferably hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C; more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

A "subsequence" refers to a sequence of nucleic acids or amino acids that comprise a part of a longer sequence of nucleic acids or amino acids (*e.g.*, protein) respectively.

Substrate: a substrate is the molecule that an enzyme naturally recognizes and converts to a product in the biochemical pathway in which the enzyme naturally carries out its function, or is a modified version of the molecule, which is also recognized by the enzyme and is converted by the enzyme to a product in an enzymatic reaction similar to the naturally-occurring reaction.

Transformation: a process for introducing heterologous DNA into a plant cell, plant tissue, or plant. Transformed plant cells, plant tissue, or plants are understood to encompass not only the end product of a transformation process, but also transgenic progeny thereof.

"Transformed," "transgenic," and "recombinant" refer to a host organism such as a bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the genome of the host or the nucleic acid molecule can also be present as an extrachromosomal molecule. Such an extrachromosomal molecule can be auto-replicating. Transformed cells, tissues, or plants are understood to encompass not only the end product of a transformation process, but also transgenic progeny thereof. A "non-transformed," "non-transgenic," or "non-recombinant" host refers to a wild-type organism, *e.g.*, a bacterium or plant, which does not contain the heterologous nucleic acid molecule.

Viability: “viability” as used herein refers to a fitness parameter of a plant. Plants are assayed for their homozygous performance of plant development, indicating which proteins are essential for plant growth.

5 I. Identification of Essential *Arabidopsis thaliana* Nucleotide Sequences and Encoded Proteins Using *Ac/Ds* Transposon or T-DNA-Mediated Mutagenesis

As shown in the examples below, the essentiality of the nucleotide sequences described herein for normal plant growth and development, have been demonstrated for the first time in *Arabidopsis* using *Ac/Ds* transposon or T-DNA-mediated mutagenesis. Having 10 established the essentiality of the function of the encoded proteins in *Arabidopsis thaliana* and having identified the nucleotide sequences encoding these essential proteins, the inventors thereby provide an important and sought after tool for new herbicide development.

Arabidopsis insertional mutant lines segregating for seedling lethal mutations are identified as a first step in the identification of essential proteins. Starting with T2 seeds 15 collected from single T1 plants containing T-DNA insertions in their genomes, those lines segregating homozygous seedling lethal seedlings are identified. *Ds* transposon insertion lines are produced as described in Sundaresan *et al.* (1995) (Genes and Dev., 9:1797-1810), incorporated herein by reference. Starting with F3 or F4 seeds collected from single F2 or F3 kanamycin-resistant plants containing *Ds* insertions in their genomes (see Figure 3 of 20 Sundaresan *et al.* (1995) (Genes and Dev., 9:1797-1810), those lines segregating homozygous seedling lethal seedlings are identified. These lines are found by placing seeds onto minimal plant growth media, which contains the fungicides benomyl and maxim, and screening for inviable seedlings after 7 and 14 days in the light at room temperature. Inviable phenotypes include altered pigmentation or altered morphology. These phenotypes are observed either on 25 plates directly or in soil following transplantation of seedlings.

Essential genes are also identified through the isolation of lethal mutants blocked in early development. Examples of lethal mutants include those blocked in the formation of the male or female gametes or embryo. Gametophytic mutants are found by examining T1 insertion lines for the presence of 50% aborted pollen grains or ovules. Embryo defective 30 mutants produce 25% defective seeds following self-pollination of T1 plants (see Errampalli *et al.* 1991, Plant Cell 3:149-157; Castle *et al.* 1993, Mol Gen Genet 241:504-514).

When a line is identified as segregating a seedling lethal or an embryo defective phenotype, it is determined if the resistance marker in the *Ds* transposon or T-DNA insertion co-segregates with the lethality (Errampalli *et al.* (1991) *The Plant Cell*, 3:149-157). Cosegregation analysis is done by placing the seeds on media containing the selective agent and scoring the seedlings for resistance or sensitivity to the agent. Examples of selective agents used are kanamycin, hygromycin, or phosphinothricin. About 35 resistant seedlings are transplanted to soil and their progeny are examined for the segregation of the seedling lethal. In the case in which the *Ds* transposon or T-DNA insertion disrupts an essential gene, there is co-segregation of the resistance phenotype and the seedling lethal or embryo defective phenotype in every plant. Therefore, in such a case, all resistant plants segregate a seedling lethal or embryo defective phenotype in the next generation; this result indicates that each of the resistant plants is heterozygous for the mutation and hemizygous for the T-DNA insert causing the mutation.

For the *Arabidopsis* lines showing co-segregation of the transposon-encoded or T-DNA-encoded resistance marker and the lethal phenotype, PCR-based molecular approaches such as, TAIL-PCR (Liu *et al.* (1995) *Plant J.*, 8:457-463; Liu and Whittier (1995), *Genomics*, 25:674-681), TAIL2k, vectorette PCR (Riley *et al.* (1990) *Nucleic Acids Research*, 18: 2887-2890), or the GenomeWalker™ kit (CLONTECH Laboratories, Inc., Palo Alto, CA), may be used to directly amplify the plant DNA fragments flanking the transposon or T-DNA. Each of these techniques utilizes the known sequence of the transposon or T-DNA, and can be used to recover small (less than 5 kb) fragments directly adjacent to the insertion. PCR products are isolated and their DNA sequence is determined.

Alternatively, plasmid rescue may be used to isolate the plant DNA/T-DNA border fragments. Southern blot analysis may be performed as an initial step in the characterization of the molecular nature of each insertion. Southern blots are done with genomic DNA isolated from heterozygotes and using probes capable of hybridizing with the T-DNA vector DNA. Using the results of the Southern analysis, appropriate restriction enzymes are chosen to perform plasmid rescue in order to molecularly clone *Arabidopsis thaliana* genomic DNA flanking one or both sides of the T-DNA insertion. Plasmids obtained in this manner are analyzed by restriction enzyme digestion to sort the plasmids into classes based on their digestion pattern. For each class of plasmid clone, the DNA sequence is determined.

The resulting sequences, obtained by any of the above outlined approaches, are analyzed for the presence of non-*Ds* transposon and non-T-DNA vector sequences, as appropriate. When such sequences are found, they are used to search DNA and protein databases using the BLAST and BLAST2 programs (Altschul *et al.* (1990) *J Mol. Biol.* 215: 5 403-410; Altschul *et al.* (1997) *Nucleic Acid Res.* 25:3389-3402, both incorporated herein by reference). Additional genomic and cDNA sequences for each gene are identified by standard molecular biology procedures.

II. Recombinant Production Of Essential Proteins And Uses Thereof

For recombinant production of a protein of the invention in a host organism, a nucleotide sequence encoding the protein is inserted into an expression cassette designed for the chosen host and introduced into the host where it is recombinantly produced. The choice of the specific regulatory sequences such as promoter, signal sequence, 5' and 3' untranslated sequence, and enhancer appropriate for the chosen host is within the level of the skill of the routineer in the art. The resultant molecule, containing the individual elements linking in the proper reading frame, is inserted into a vector capable of being transformed into the host cell. Suitable expression vectors and methods for recombinant production of proteins are well known for host organisms such as *E. coli*, yeast, and insect cells (see, *e.g.*, Lucknow and Summers, *Bio/Technol.* 6:47 (1988)). Additional suitable expression vectors are baculovirus expression vectors, *e.g.*, those derived from the genome of *Autographica californica* nuclear polyhedrosis virus (AcMNPV). A preferred baculovirus/insect system is PVL1392(3) used to transfect *Spodoptera frugiperda* SF9 cells (ATCC) in the presence of linear *Autographica californica* baculovirus DNA (Phramingen, San Diego, CA). The resulting virus is used to infect HighFive *Tricoplusia ni* cells (Invitrogen, La Jolla, CA).

Recombinantly produced proteins are isolated and purified using a variety of standard techniques. The actual techniques used vary depending upon the host organism used, whether the protein is designed for secretion, and other such factors. Such techniques are well known to the skilled artisan (*see, e.g.* chapter 16 of Ausubel, F. *et al.*, "Current Protocols in Molecular Biology", pub. by John Wiley & Sons, Inc. (1994)).

III. Assays For Characterizing The Essential Proteins

The recombinantly produced proteins described herein are useful for a variety of purposes. For example, they can be used in *in vitro* assays to screen known herbicidal chemicals whose target has not been identified to determine if they inhibit protein activity.

5 Such *in vitro* assays may also be used as more general screens to identify chemicals that inhibit such protein activity and that are therefore novel herbicide candidates. Recombinantly produced proteins may also be used to elucidate the complex structure of these molecules and to further characterize their association with known inhibitors in order to rationally design new inhibitory herbicides. Alternatively, the recombinant protein can be used to isolate 10 antibodies or peptides that modulate the activity and are useful in transgenic solutions.

IV. *In vitro* Inhibitor Assay: Discovery of Small Molecule Ligands That Interact with Essential Proteins Of Unknown Biochemical Function

Once a protein has been identified as a potential herbicide target based on its 15 essentiality for normal plant growth and viability, a next step is to develop an assay that allows screening large number of chemicals to determine which ones interact with the protein. Although it is straightforward to develop assays for proteins of known function, developing assays with proteins of unknown functions can be more difficult.

To address this issue, novel technologies are used that can detect interactions between 20 a protein and a compound without knowing the biological function of the protein. A short description of three methods is presented, including fluorescence correlation spectroscopy, surface-enhanced laser desorption/ionization, and biacore technologies.

Fluorescence Correlation Spectroscopy (FCS) theory was developed in 1972 but it is only in recent years that the technology to perform FCS became available (Madge *et al.* 25 (1972) Phys. Rev. Lett., 29: 705-708; Maiti *et al.* (1997) Proc. Natl. Acad. Sci. USA, 94: 11753-11757). FCS measures the average diffusion rate of a fluorescent molecule within a small sample volume. The sample size can be as low as 10^3 fluorescent molecules and the sample volume as low as the cytoplasm of a single bacterium. The diffusion rate is a function of the mass of the molecule and decreases as the mass increases. FCS can therefore be 30 applied to protein-ligand interaction analysis by measuring the change in mass and therefore in diffusion rate of a molecule upon binding. In a typical experiment, the target to be analyzed is expressed as a recombinant protein with a sequence tag, such as a poly-histidine

sequence, inserted at the N or C-terminus. The expression takes place in *E. coli*, yeast or insect cells. The protein is purified by chromatography. For example, the poly-histidine tag can be used to bind the expressed protein to a metal chelate column such as Ni²⁺ chelated on iminodiacetic acid agarose. The protein is then labeled with a fluorescent tag such as 5 carboxytetramethylrhodamine or BODIPY® (Molecular Probes, Eugene, OR). The protein is then exposed in solution to the potential ligand, and its diffusion rate is determined by FCS using instrumentation available from Carl Zeiss, Inc. (Thornwood, NY). Ligand binding is determined by changes in the diffusion rate of the protein.

Surface-Enhanced Laser Desorption/Ionization (SELDI) was invented by Hutchens 10 and Yip during the late 1980's (Hutchens and Yip (1993) *Rapid Commun. Mass Spectrom.* 7: 576-580). When coupled to a time-of-flight mass spectrometer (TOF), SELDI provides a mean to rapidly analyze molecules retained on a chip. It can be applied to ligand-protein interaction analysis by covalently binding the target protein on the chip and analyze by MS 15 the small molecules that bind to this protein (Worrall *et al.* (1998) *Anal. Biochem.* 70: 750-756). In a typical experiment, the target to be analyzed is expressed as described for FCS. The purified protein is then used in the assay without further preparation. It is bound to the SELDI chip either by utilizing the poly-histidine tag or by other interaction such as ion 20 exchange or hydrophobic interaction. The chip thus prepared is then exposed to the potential ligand via, for example, a delivery system capable to pipette the ligands in a sequential manner (autosampler). The chip is then submitted to washes of increasing stringency, for example a series of washes with buffer solutions containing an increasing ionic strength. After each wash, the bound material is analyzed by submitting the chip to SELDI-TOF. Ligands that specifically bind the target will be identified by the stringency of the wash 25 needed to elute them.

25 Biacore relies on changes in the refractive index at the surface layer upon binding of a ligand to a protein immobilized on the layer. In this system, a collection of small ligands is injected sequentially in a 2-5 microlitre cell with the immobilized protein. Binding is detected by surface plasmon resonance (SPR) by recording laser light refracting from the surface. In general, the refractive index change for a given change of mass concentration at the surface 30 layer, is practically the same for all proteins and peptides, allowing a single method to be applicable for any protein (Liedberg *et al.* (1983) *Sensors Actuators* 4: 299-304; Malmquist (1993) *Nature*, 361: 186-187). In a typical experiment, the target to be analyzed is expressed

as described for FCS. The purified protein is then used in the assay without further preparation. It is bound to the Biacore chip either by utilizing the poly-histidine tag or by other interaction such as ion exchange or hydrophobic interaction. The chip thus prepared is then exposed to the potential ligand via the delivery system incorporated in the instruments sold by Biacore (Uppsala, Sweden) to pipette the ligands in a sequential manner (autosampler). The SPR signal on the chip is recorded and changes in the refractive index indicate an interaction between the immobilized target and the ligand. Analysis of the signal kinetics on rate and off rate allows the discrimination between non-specific and specific interaction.

Another assay for small molecule ligands that interact with a polypeptide is an inhibitor assay. For example, such an inhibitor assay useful for identifying inhibitors of the products of essential plant nucleic acid sequences, such as the essential *Arabidopsis* proteins described herein, comprises the steps of:

- a) reacting an essential *Arabidopsis* protein described herein and a substrate thereof in the presence of a suspected inhibitor of the protein's function;
- b) comparing the rate of enzymatic activity of the protein in the presence of the suspected inhibitor to the rate of enzymatic activity under the same conditions in the absence of the suspected inhibitor; and
- c) determining whether the suspected inhibitor inhibits the essential *Arabidopsis* protein.

For example, the inhibitory effect on the activity of a herein-described essential *Arabidopsis* protein, may be determined by a reduction or complete inhibition of protein activity in the assay. Such a determination may be made by comparing, in the presence and absence of the candidate inhibitor, the amount of substrate used or intermediate or product made during the reaction.

V. Production of peptides

Phage particles displaying diverse peptide libraries permits rapid library construction, affinity selection, amplification and selection of ligands directed against an essential protein (H.B. Lowman, *Annu. Rev. Biophys. Biomol. Struct.* 26, 401-424 (1997)). Structural analysis of these selectants can provide new information about ligand-target molecule interactions and

then in the process also provide a novel molecule that can enable the development of new herbicides based upon these peptides as leads.

VI. *In Vivo* Inhibitor Assay

5 In one embodiment, a suspected herbicide, for example identified by *in vitro* screening, is applied to plants at various concentrations. The suspected herbicide is preferably sprayed on the plants. After application of the suspected herbicide, its effect on the plants, for example death or suppression of growth is recorded.

10 In another embodiment, an *in vivo* screening assay for inhibitors of the activity of a hereindescribed essential protein uses transgenic plants, plant tissue, plant seeds or plant cells capable of overexpressing a nucleotide sequence disclosed herein that encodes an essential protein, wherein the essential protein is enzymatically active in the transgenic plants, plant tissue, plant seeds or plant cells. A chemical is then applied to the transgenic plants, plant tissue, plant seeds or plant cells and to the isogenic non-transgenic plants, plant tissue, plant 15 seeds or plant cells, and the growth or viability of the transgenic and non-transformed plants, plant tissue, plant seeds or plant cells are determined after application of the chemical and compared. Compounds capable of inhibiting the growth of the non-transgenic plants, but not affecting the growth of the transgenic plants are selected as specific inhibitors of the essential protein's activity.

20 The invention will be further described by reference to the following detailed examples. These examples are provided for purposes of illustration only, and are not intended to be limiting unless otherwise specified.

EXAMPLES

25 Standard recombinant DNA and molecular cloning techniques used here are well known in the art and are described by J. Sambrook, *et al.*, *Molecular Cloning: A Laboratory Manual*, 3d Ed., Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press (2001); by T.J. Silhavy, M.L. Berman, and L.W. Enquist, *Experiments with Gene Fusions*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1984) and by Ausubel, F.M. *et al.*, *Current 30 Protocols in Molecular Biology*, New York, John Wiley and Sons Inc., (1988), Reiter, *et al.*, *Methods in Arabidopsis Research*, World Scientific Press (1992), and Schultz *et al.*, *Plant Molecular Biology Manual*, Kluwer Academic Publishers (1998). These references describe

the standard techniques used for all steps in tagging and cloning genes from *Ac/Ds* transposon or T-DNA mutagenized populations of *Arabidopsis*: plant infection and transformation; screening for the identification of seedling mutants; and cosegregation analysis. *Ds* transposon insertion lines produced as described in Sundaresan *et al.* (1995) *Genes and Dev.*, 9:1797-1810) are used in these experiments. T-DNA lines are generated using vacuum infiltration or floral dip methods (Bechtold *et al.* (1993) *C. R. Acad. Sci. Paris*, 316:1194-1199; Clough and Bent (1998) *Plant J.*, 16:735-743; Desfeux *et al.* (2000) *Plant Physiol.*, 123:895-904).

10 Example 1: Identification of *Arabidopsis* Mutants with Lethal Phenotypes

Essential genes are identified through the isolation of lethal mutants blocked in early development. Examples of lethal mutants include those blocked in the formation of the male or female gametes, embryo, or resulting seedling. Gametophytic mutants are found by examining insertion lines for the presence of 50% aborted pollen grains or ovules. Embryo defective lethal mutants usually produce 25% defective seeds following self-pollination of plants heterozygous for an insertion (see Errampalli *et al.* 1991, *Plant Cell* 3:149-157; Castle *et al.* 1993, *Mol Gen Genet* 241:504-514). Seedling lethal mutants usually segregate 25% seedlings that exhibit a lethal phenotype.

20 Example 2: Cosegregation Analysis for Lines with Lethal Phenotypes

The linkage of the mutation to the *Ds* or T-DNA insertion is established after identifying a transformed line segregating for a lethal phenotype of interest. A line segregating with a single functional insert will segregate for resistance in the ratio of about 2:1 (resistant: sensitive) to the selectable marker. In the case of an embryo defective mutant, one-quarter of the progeny of a plant heterozygous for an insertion will fail to germinate due to embryo lethality, resulting in a reduction of the normal 3:1 ratio to 2:1. In the case of a seedling lethal mutant, the seedlings with a mutant phenotype are excluded in the calculation of this ratio. Each of the resistant progeny is therefore heterozygous for the mutation if the *Ds* or T-DNA insertion is causing the mutant phenotype. To establish cosegregation of the insertion and the mutant phenotype, about 30 resistant progeny are transplanted to soil and each plant is shown to segregate the 25% progeny with a lethal phenotype by the appropriate screening of embryo or seedlings. When all resistant plants segregate the lethal phenotype,

there is cosegregation of the insertion and the lethal mutation and the line is designated as "tagged."

Example 3: T-DNA Border Isolation by Plasmid Rescue

5 The plasmid rescue technique is used to molecularly clone *Arabidopsis* flanking DNA from one or both sides of the T-DNA insertion(s). *Arabidopsis* genomic DNA is isolated as described by Reiter *et al.* in *Methods in Arabidopsis Research*, World Scientific Press (1992). Genomic DNA is digested with a restriction endonuclease and ligated overnight. After ligation, the DNA is transformed into competent *E. coli* strain XL-1 Blue, DH10B, DH5
10 alpha, or the like, and colonies are selected on semi-solid medium containing ampicillin. Resistant colonies are picked into liquid medium with ampicillin and grown overnight. Plasmid DNA is isolated and digested with the rescue enzyme and analyzed on agarose gels containing ethidium bromide for visualization. Plasmids that represent different size classes are sequenced using primers that flank the plant DNA portion of the rescue element and the
15 sequence is analyzed to determine what portion is plant DNA and what gene has been disrupted. The plasmid rescue is validated via PCR of template genomic DNA from a heterozygote for the insertion mutation. The experiment uses a primer anchored in the predicted flanking sequence and a primer in the T-DNA insertion. Finding a PCR product of the appropriate size, based on the sequence of the plasmid rescue clone confirms a valid
20 rescue. Alternatively, Southern blot analysis with a probe that detects the relevant region of *Arabidopsis* DNA in genomic DNA from a heterozygote for the insertion mutation can be used to confirm the plasmid rescue results.

Example 4: Transposon or T-DNA Border Isolation by TAIL-PCR

25 *Arabidopsis* genomic DNA is isolated according to Reiter *et al.* in *Methods in Arabidopsis Research*, World Scientific Press (1992) or using the Nucleon PhytoPure™ Plant DNA isolation kit (Amersham International plc, Buckinghamshire, England) or the Puregene DNA isolation kit (Gentra Systems, Minneapolis, MN). Fragments of genomic DNA flanking the borders of the transposon or T-DNA are isolated using the TAIL-PCR technique (Liu *et*
30 *al.* (1995) Plant J., 8:457-463; Liu and Whittier (1995), Genomics, 25:674-681). Three sets of 12 TAIL-PCR reactions, referred to as the primary, secondary and tertiary reactions, are performed. In each reaction, one arbitrary degenerate primer and one transposon-specific or

T-DNA-specific primer are used. The arbitrary degenerate primer is chosen from among seven primers, LWAD1, CA50, CA51, CA52, CA53, CA54, and CA55 (Table 1), which are used to prime the genomic DNA flanking the insertion. Alternatively, less than 12 TAIL-PCR reactions are done using fewer arbitrary degenerate primers. These degenerate primers 5 are used in combination with two sets of three, nested, transposon-specific primers (Table 2) or T-DNA-specific primers (Table 3). The transposon-specific primers are homologous to regions of the *Ds* elements that lie at the outermost ends of the transposons, DS5 at the 5' end (primers 5A, 5B, and 5C) and DS3 at the 3' end (primers 3A, 3B, and 3C). The T-DNA-specific primers are homologous to regions of the T-DNA that lie in the borders of the T- 10 DNAs. For the pCSA104 and pDAP101 T-DNAs, right borders are recovered with CA66 (primary primer), CA67 (secondary primer), and CA68 (tertiary primer) and left borders are recovered with JM33 (tertiary primer); JM34 (secondary primer); and JM35 (primary primer). For the pCSA110 T-DNA, right borders are recovered with QRB1 (primary primer), QRB2 (secondary primer), and QRB3 (tertiary primer) and left borders are recovered with JM33 15 (tertiary primer); JM34 (secondary primer); and JM35 (primary primer). For the pPCV1CEn4HPT (Hayashi *et al.* (1992), Science, 258:1350-1353) and pSKI015 (Weigel *et al.* (2000) Plant Physiol. 122:1003-1014) T-DNAs, left borders are recovered with SKI1 (primary primer), SKI2 (secondary primer), and SKI3 (tertiary primer). When the degenerate and nested primer pairs are used in a series of low and high-stringency PCR amplifications, as 20 described in the TAIL-PCR protocol (Liu and Whittier (1995), Genomics, 25:674-681), DNA fragments are produced that correspond to the genomic DNA that is directly adjacent to the transposon or T-DNA insertion. The nucleic acid sequences of the PCR products from the tertiary TAIL-PCR reactions are then determined by standard molecular biology techniques. The resulting sequences are analyzed for the presence of non-*Ds* transposon or non-T-DNA 25 vector sequence.

To confirm the integrity of the resultant products, PCR primers specific to the flanking genomic region are designed and used in conjunction with the tertiary nested primer in a PCR reaction, to confirm the transposon or T-DNA insertion point within the genomic DNA. Finding a PCR product of the appropriate size, based on the sequence of the TAIL-PCR clone 30 confirms a valid rescue.

Table 1: Arbitrary Degenerate Primers

<u>SEQ ID NO:</u>	<u>Primer</u>	<u>Degen.</u>	<u>Primer Sequence</u>
101	LWAD1	1026	ngt tgw gna twt sgw gnt
102	CA50	128	ngt cga swg ana wga a
5	103	CA51	tgw gna gsa nca sag a
	104	CA52	agw gna gwa nca wag g
	105	CA53	stt gnt ast nct ntg c
	106	CA54	ntc gas twt sgw gtt
	107	CA55	wgt gna gwa nca nag a

10

Table 2: Nested Primers For *Ds* Lines

<u>SEQ ID NO:</u>	<u>Primer</u>	<u>Primer Sequence</u>
108	5A	actagctctaccgttccgttccgtttac
109	5B	ttacctcgggttcgaatcgatcggataaa
15	110	aaaatcggttatacgataacggtcggtacggga
	111	gggtcttgcggatctgaatataatgtttcatgtgt
	112	taccgaagaaaaataccggtcccgtccgatttcgac
	113	ggatcgatcggtttcgattaccgtatttatcc

20

Table 3: Nested Primers For T-DNA Lines

<u>SEQ ID NO:</u>	<u>Primer</u>	<u>Primer Sequence</u>
114	CA66	att agg cac ccc agg ctt tac act tta tg
115	CA67	gta tgt tgt gtg gaa ttg tga gcg gat aac
116	CA68	taa caa ttt cac aca gga aac agc tat gac
25	117	tag cat ctg aat ttc ata acc aat ctc gat aca c
	118	gct tcc tat tat atc ttc cca aat tac caa tac a
	119	gcc ttt tca gaa atg gat aaa tag cct tgc ttc c
	120	caa act agg ata aat tat cgc gcg cgg tgt ca
	121	ggt gtc atc tat gtt act aga tcg gga att ga
30	122	cgc cat ggc ata tgc tag cat gca taa ttc
	123	aat tgg taa tta ctc ttt ctt ttc ctc cat att ga
	124	ata ttg acc atc ata ctc att gct gat cca t
	125	tga tcc atg tag att tcc cgg aca tga a

Example 5: Transposon or T-DNA Border Isolation by TAIL2k PCR

Arabidopsis genomic DNA is isolated according to Reiter *et al.* in Methods in *Arabidopsis* Research, World Scientific Press (1992) or using the Nucleon PhytoPure™ Plant

5 DNA isolation kit (Amersham International plc, Buckinghamshire, England) or the Puregene DNA isolation kit (Gentra Systems, Minneapolis, MN). Fragments of genomic DNA flanking the borders of the transposon or T-DNA are isolated using the TAIL2k PCR technique. Two sets of 12 TAIL-PCR reactions, referred to as the primary and secondary reactions, are performed. In each reaction, one arbitrary degenerate primer and one transposon-specific or
10 T-DNA-specific primer are used. The arbitrary degenerate primer is selected from among six primers; CA50, CA51, CA52, CA53, CA54, and CA55 (Table 1), which are used to prime the genomic DNA flanking the insertion. Alternatively, less than 12 TAIL-PCR reactions are done using fewer arbitrary degenerate primers. These degenerate primers are used in combination with two sets of two, nested, transposon-specific primers (Table 2) or T-DNA-specific primers (Table 3). The transposon-specific primers are homologous to regions of the *Ds* elements that lie at the outermost ends of the transposons, DS5 at the 5' end (primers 5A, 15 5B, and 5C) and DS3 at the 3' end (primers 3A, 3B, and 3C). The T-DNA-specific primers are homologous to regions of the T-DNA that lie in the borders of the T-DNAs. For the pCSA104 and pDAP101 T-DNAs, right borders are recovered with CA66 (primary primer), CA67 (secondary primer), and CA68 (sequencing primer) and left borders are recovered with JM33 (sequencing primer), JM34 (secondary primer), and JM35 (primary primer). Primers CA66, CA67, and CA68 are also known as RB1, RB2, and RB3, respectively. Primers JM35, 20 JM34, and JM33 are also known as LB1, LB2, and LB3, respectively. For the pCSA110 T-DNA, right borders are recovered with QRB1 (primary primer), QRB2 (secondary primer), and QRB3 (sequencing primer) and left borders are recovered with JM33 (sequencing primer); JM34 (secondary primer); and JM35 (primary primer). For the pPCV1CEn4HPT (Hayashi *et al.* (1992), *Science*, 258:1350-1353) and pSKI015 (Weigel *et al.* (2000) *Plant Physiol.* 122:1003-1014) T-DNAs, left borders are recovered with SKI1 (primary primer), SKI2 (secondary primer), and SKI3 (sequencing primer). When the degenerate and nested
25 primer pairs are used in a series of low and high-stringency PCR amplifications, as described in the TAIL-PCR protocol (Liu and Whittier (1995), *Genomics*, 25:674-681), DNA fragments are produced that correspond to the genomic DNA that is directly adjacent to the transposon
30

or T-DNA insertion. TAIL2k-PCR differs from the original TAIL-PCR protocol by the elimination of the tertiary PCR and modification of the secondary PCR. The cycling conditions used in the secondary reaction are modified to include 5 high annealing temperature cycles (64 degrees C) at the beginning, three additional so-called super cycles, 5 and five additional low annealing temperature cycles (44 degrees C) at the end of the reaction. The melting and extension times are the same as all other TAIL-PCR reactions. Additionally, the reaction volume is increased to 40 microliters. The nucleic acid sequences of the PCR products from the secondary TAIL2k-PCR reactions are then determined by standard molecular biology techniques. The resulting sequences are analyzed for the presence of non-10 *Ds* transposon or non-T-DNA vector sequence.

To confirm the integrity of the resultant products, PCR primers specific to the flanking genomic region are designed and used in conjunction with the tertiary nested primer in a PCR reaction, to confirm the transposon or T-DNA insertion point within the genomic DNA. Finding a PCR product of the appropriate size, based on the sequence of the TAIL2k-PCR 15 sequencing result confirms a valid rescue.

Example 6: Identification of Both Borders of a T-DNA or *Ds* Insertion

If the results of border rescue provide information on only one of the two borders for an insertion in a given line, additional experiments are performed to identify the second 20 border. These experiments are necessary to show that a single gene has been disrupted in a given line. In some cases, an insertion can affect more than a single gene due to a chromosomal deletion or rearrangement. In those cases, additional experiments are required to identify which of the affected genes is responsible for the lethal phenotype.

When both borders of an insertion are not recovered, primers are designed to isolate a 25 PCR product that will provide information on the location of the missing border. Three primers are chosen in *Arabidopsis* genomic DNA on the opposite side of the insertion about one, two, and five kb away from the insertion point; the primers point towards the expected second border. Long PCR conditions (Advantage 2, Clontech) are then employed following the manufacturer's directions to amplify the relevant region from genomic DNA isolated from 30 a heterozygote for the lethal mutation. PCR reactions are performed using appropriate pairs of genomic and T-DNA or *Ds* border primers. Finding a PCR product of the appropriate size,

based on the sequence of the TAIL-PCR clone confirms a valid rescue of the second border. In some cases, the PCR product is directly sequenced to determine the exact insertion point.

If the second border is not recovered with this method, an additional set of PCR reactions are preformed. In these experiments, the genomic primers are paired with a series of 5 internal T-DNA or *Ds* primers designed at about one kb intervals in both orientations across the entire T-DNA or *Ds* vector sequence. Finding a PCR product of the appropriate size, based on the sequence of the TAIL-PCR clone confirms a valid rescue of the second border. In some cases, the PCR product is directly sequenced to determine the exact insertion point. Any borders recovered with this approach are classified as abnormal because they lack the 10 ends of the *Ds* transposon or the expected 24 bp T-DNA imperfect repeat characteristic of right and left borders.

Example 7: Identification of Insertion Points for Lines with Lethal Phenotypes

For each line with a lethal phenotype, the sequences of the borders of the insertion are 15 determined and the insertion points in the *Arabidopsis* genome are deduced. For *Ds* insertion lines, PCR products are obtained from the *Ds3* and *Ds5* borders. For T-DNA lines, PCR products or plasmid rescue clones are obtained from left (LB), right (RB), or abnormal (AB) borders. These sequences are used in BLASTn searches against nucleotide databases (Altschul *et al.* (1990) J Mol. Biol. 215:403-410; Altschul *et al.* (1997) Nucleic Acids Res. 25:3389-3402). The results are summarized in Table 4. *Ds* line names begin with ET or GT; T-DNA line names are numbers. The insertion point (Insert Pt.) and the direction of the flanking sequence (Dir.) either up (U) or down (D) in the genome section is noted. Often, small deletions or duplications of genomic DNA accompany the insertion of a T-DNA or *Ds* transposon.

25 The gene that has been inactivated in a given line with a lethal phenotype is determined from the insertion points for that line. Often, the precise location of an ORF for a given gene is not known, but predictions are available in genome sections deposited in GenBank. The precise boundaries of that ORF is determined as described in Example 7.

30 Table 4: Insertion Points For Lines With Lethal Phenotypes

Gene	Line #	Border	Genome Section	Acc. #	Insert Pt.	Dir.
942	942	LB	K24G6	AB012242	33667	D

978	978	LB	F23N20	AC016972	58221	D
	978	LB	F23N20	AC016972	58301	U
3218	3218	LB	T8K14	AC007202	10500	D
	3218	LB	T8K14	AC007202	10540	U
4563	4563	LB	ATCHRII092	AC006438	25542	D
8794	8794	LB	F2J6	AC009526	45854	D
	8794	LB	F2J6	AC009526	45879	U
9106	9106	LB	T2J13	AL132967	78013	U
	9106	AB	T2J13	AL132967	77943	D
10708	10708	RB	F1I21	AC005687	40005	D
	10708	LB	F1I21	AC005687	40042	U
70241	70241	LB	F1I21	AC005687	40210	D
	70241	RB	F1I21	AC005687	40215	U
10844	10844	LB	F13F21	AC007504	60873	U
	10844	LB	F13F21	AC007504	60839	D
10951	10951	LB	MKP11	AB005238	20298	D
	10951	LB	MKP11	AB005238	20318	U
12935	12935	LB	ATCHRII150	AC005168	36510	D
	12935	LB	ATCHRII150	AC005168	36545	U
13823	11361	LB	T27G7	AC006932	78096	U
	11361	AB	T27G7	AC006932	78065	D
	13823	LB	T27G7	AC006932	78096	U
	13823	RB	T27G7	AC006932	77722	D
14519	14519	LB	ATCHRIV72	AL161576	50259	U
	14519	AB	ATCHRIV72	AL161576	50228	D
14610.1	14610.1	LB	F4P13	AC009325	55319	U
	14610.1	RB	F4P13	AC009325	55442	D
14891	14891	LB	ATCHRIV89	AL161593	11412	U
	14891	RB	ATCHRIV89	AL161593	11313	D
14986	14986	LB	K10D20	AP000410	51816	D
	14986	RB	K10D20	AP000410	54505	U
15377	15377	RB	F28G11	AC074025	19572	D
	15377	LB	F28G11	AC074025	19587	U
16219	16219	LB	MRO11	AB005244	51998	U
	16219	LB	MRO11	AB005244	51995	D
16547	16547	LB	ATCHRIV65	AL161565	80692	D
	16547	RB	ATCHRIV65	AL161565	80791	U
20933	20933	LB	ATCHRII146	AC004747	47678	D
	20933	LB	ATCHRII146	AC004747	47683	U
21455	21455	LB	ATCHRIV54	AL161554	105596	U
	21455	RB	ATCHRIV54	AL161554	105542	D
21878	21878	LB	T19F11	AC009918	19609	D
23915	23915	LB	ATCHRII008	AC005936	49629	D
	23915	LB	ATCHRII008	AC005936	49657	U
30945	30945	LB	ATCHRII192	AC004238	2411	D
	30945	LB	ATCHRII192	AC004238	2410	U

31895	31895	LB	MTI20	AB013396	52020	D
	31895	LB	MTI20	AB013396	52089	U
34269	34269	LB	T4O12	AC007396	92811	U
	34269	RB	T4O12	AC007396	92808	D
34540	34540	LB	T1G11	AC002376	41572	D
	34540	LB	T1G11	AC002376	41608	U
72902	72902	LB	T1G11	AC002376	41494	U
	72902	LB	T1G11	AC002376	41465	D
34555	34555	LB	T1F15	AC004393	42152	D
	54334	RB	T1F15	AC004393	41803	U
	54334	LB	T1F15	AC004393	41671	D
35154	35154	RB	MWD9	AB007651	45718	D
	35154	LB	MWD9	AB007651	45732	U
35438	35438	LB	MAL21	AP000383	25170	D
	35438	LB	MAL21	AP000383	25738	U
37351	37351	LB	F25C20	AC007296	52890	U
	37351	RB	F25C20	AC007296	52196	D
37389	37389	LB	F3F19	AC007357	45488	U
	37389	RB	F3F19	AC007357	45471	D
38108	38108	LB	ATCHRII150	AC005168	83430	D
	38108	RB	ATCHRII150	AC005168	83446	U
43301	43301	RB	T22D16	AL357612	57549	D
	43301	LB	T22D16	AL357612	57599	U
46250	46250	LB	F17A9	AC016827	74222	D
	46250	RB	F17A9	AC016827	74274	U
47050A	47050	LB	T23E18	AC009978	49445	D
	47050	RB	T23E18	AC009978	49475	U
52949A	52949	LB	K16H17	AB016884	34713	D
	52949	LB	K16H17	AB016884	34718	U
53210A	53210	RB	ATCHRII017	AC007167	92796	D
	53210	LB	ATCHRII017	AC007167	92942	U
69121	69121	LB	ATCHRII017	AC007167	94478	D
	69121	LB	ATCHRII017	AC007167	94502	U
55483	55483	RB	ATCHRII164	AC005727	71269	U
	55483	LB	ATCHRII164	AC005727	71258	D
58351A	58351	RB	MYH9	AB016893	42547	D
	58351	LB	MYH9	AB016893	42772	U
60944	60944	LB	F1B16	AC023754	89492	U
	60944	LB	F1B16	AC023754	89428	D
62837	62837	LB	T21J18	AL132963	70906	U
	62837	LB	T21J18	AL132963	70873	D
65310	65310	LB	T20H2	AC022472	8158	U
	65310	RB	T20H2	AC022472	8096	D
68181	68181	RB	F12A12	AL133314	38270	U
	68181	LB	F12A12	AL133314	38275	D
70913	70913	LB	T24H18	AL353013	5347	D

	70913	LB	T24H18	AL353013	5358	U
71067	71067	LB	F2E2	AC069252	63031	U
	71067	LB	F2E2	AC069252	62932	D
71654	71654	RB	MYA6	AB023046	71956	U
	71654	LB	MYA6	AB023046	71907	D
ET3172	ET3172	DS5	ATCHRIV4	AL161492	134442	U
ET3546	ET3546	DS3	ATCHRII115	AC006081	20874	D
	ET3546	DS5	ATCHRII115	AC006081	20973	U

Example 8: Identification of cDNAs for Essential Genes

A cDNA for a gene identified as essential is identified using a variety of approaches. This information enables the ORF for a given gene to be identified and used for other 5 experiments including expression of the corresponding protein in heterologous systems.

If there is a full-length cDNA deposited in GenBank or published elsewhere, that sequence may be checked independently using methods described below. Alternatively, the sequence may be considered to be correct.

In some cases, there are published EST sequences that can be assembled to cover the 10 entire ORF from start codon to stop codon. This sequence may be checked independently using methods described below or it may be considered to be correct.

Often part of the cDNA is published and this information can be used to identify the entire ORF. If the 5' end containing the start codon is known, 3' RACE is performed to identify the remainder of the cDNA. If the 3' end containing the stop codon is known, 5' 15 RACE is performed to identify the remainder of the cDNA. If both the 5' and the 3' ends are known, but the sequence between the two ends of the cDNA is not known, PCR is performed with primers hybridizing to each end of the cDNA. In all three of these cases, PCR is performed using template DNA from a GeneRacer (Invitrogen) or a Marathon (Clontech) cDNA library prepared from RNA isolated from seedling tissue. A resulting PCR product is 20 TA-cloned (Original TA-Cloning kit, Invitrogen) and sequenced.

If no part of the cDNA is published, the cDNA is identified by starting from gene model predictions in the annotation for genomic clones or elsewhere. To identify the ORF, primers are designed to the 5' and 3' ends of the predicted ORF. PCR is performed using template DNA from a cDNA library prepared from seedling tissue or the pFL61 *Arabidopsis* 25 cDNA library (Minet *et al.* (1992) Plant J. 2: 417-422). The resulting PCR product is TA-cloned (Original TA-Cloning kit, Invitrogen) and sequenced. Alternatively, 5' and 3' RACE are performed with primers predicted by gene models to be in exons. PCR is performed using

template DNA from a GeneRacer (Invitrogen) or a Marathon (Clontech) cDNA library prepared from RNA isolated from seedling tissue. A resulting PCR product is TA-cloned (Original TA-Cloning kit, Invitrogen) and sequenced.

5 If the cDNA sequence is the same as the sequence predicted in the GenBank annotation, the experiments confirm for the first time the actual ORF. If the cDNA sequence is not the same as the sequence predicted in the GenBank annotation, the experiments identify for the first time the actual ORF. In some cases, more than one cDNA sequence is found for a given gene and both sequences are included in this application.

10 Example 9: Description of Essential Genes

The putative function of the protein encoded by each essential gene is determined from analysis of the ORF in each cDNA. Information from the relevant *Arabidopsis* genomic section deposited in GenBank is used as a starting point to explore the function of a given gene. This analysis also includes BLAST searches (Altschul *et al.* (1990) *J. Mol. Biol.*

15 215:403-410; Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402) of sequence databases to identify similar proteins. Table 5 describes the putative functions for the essential genes discovered in this application.

Table 5: Putative Functions For Essential Genes

20

Gene	SEQ ID Nos:	Putative Function & Similar Genes	References
00942	1-2	similarity to disease resistance protein large gene family in <i>Arabidopsis</i> including disease resistance proteins RPP1-WsA,B&C; similar to tobacco TMV resistance protein N	Whitham, S. <i>et al.</i> (1994) <i>Cell</i> 78:1101-1115; Botella, M.A., <i>et al.</i> (1998) <i>Plant Cell</i> 10: 1847-1860
00978	3-4	unknown protein similar to <i>Arabidopsis</i> protein of unknown function (CAB87660) & ESTs from many plants	none
03218	5-6	AAA ATPase similar to <i>E. coli</i> FtsH cell division protein (P28691) that acts as an ATP-dependent metallopeptidase; homologs in many species	Schumann, W. (1999) <i>FEMS Microbiol Rev</i> 23:1-11; Langer, T. (2000) <i>Trends Biochem Sci</i> 2000 25:247-251

04563	7-8	unknown protein large gene family in <i>Arabidopsis</i> of unknown function proteins	none
08794	9-10	putative histidine decarboxylase similar to Brassica, tomato (tom92), and rice putative histidine decarboxylases	Picton, S <i>et al.</i> (1993) <i>Plant Mol Biol</i> 23:627-631; Watanabe, T <i>et al.</i> (1990) <i>Trends Pharmacol Sci</i> 11:363-367; Vaaler, G.L. & Snell, E.E. (1989) <i>Biochemistry</i> 28:7306-7313
09106	11-12	cytosolic 40S ribosomal protein S11-alpha	Browning, K.S. (1996) <i>Plant Mol Biol</i> 32:107-144; Gantt, J. S. & Thompson, M.D. (1990) <i>J. Biol Chem</i> 265:2763-2767
10708	13-14	cytoplasmic 60S ribosomal protein L3	Peltz, S.W. <i>et al.</i> (1999) <i>Mol Cell Biol</i> 19:384-391; Kim, Y. <i>et al.</i> (1990) <i>Gene</i> 93:177-182; Wickner, R.B <i>et al.</i> (1982) <i>Proc Natl Acad Sci USA</i> 79:4706-4708
10844	15-16	40S ribosomal protein S17-like	Gantt, J.S. & Thompson, M.D. (1990) <i>J Biol Chem</i> 265:2763-2767; Wiener, L. <i>et al.</i> (1988) <i>Nucleic Acids Res</i> 16:1233-1250
10951	17-18	phytoene synthase	Welsch, R. <i>et al.</i> (2000) <i>Planta</i> 211:846-854; Shewmaker, C.K. <i>et al.</i> (1999) <i>Plant J.</i> 20:401-412; Von Lintig, J. <i>et al.</i> (1997) <i>Plant J.</i> 12:625-634
12935	19-20	putative choline kinase similar to soybean choline kinase (T08815) and mouse & human choline/ethanolamine kinases	Monks, D.E. <i>et al.</i> (1996) <i>Plant Physiol.</i> 110:1197-1205; Bligny, R. <i>et al.</i> (1989) <i>J Biol Chem.</i> 264:4888-4895; Wharfe, J. & Harwood, J.L. (1979) <i>Biochim Biophys Acta.</i> 575:102-111
13823	21-22	magnesium protoporphyrin IX chelatase subunit D	Papenbrock, J. <i>et al.</i> (1997) <i>Plant J.</i> 12:981-990; Papenbrock, J. <i>et al.</i> (2000) <i>Plant Physiol.</i> 122:1161-1169; Luo, M. <i>et al.</i> (1999) <i>Plant Mol Biol.</i> 41:721-731; Jensen, P.E. <i>et al.</i> (1996) <i>Mol. Gen. Genet.</i> 250:383-394

14519	23-24	putative protein small gene family in <i>Arabidopsis</i> of unknown function proteins	none
14610.1	25-26	putative cell division control protein; similar to cdc48, AAA ATPase proteins similar to <i>S. pombe</i> AAA ATPase (CAB16902); <i>Arabidopsis</i> cdc48 homolog (P54609); cdc48/valosin- containing protein homologs from soybean, <i>Capsicum annuum</i> , rice, <i>Dictyostelium</i> ; <i>Drosophila</i> smallminded	Frohlich, K.U. <i>et al.</i> (1991) J Cell Biol. 114:443-453; Feiler, H.S. <i>et al.</i> (1995) EMBO J. 14:5626-5637; Langer, T. (2000) Trends Biochem Sci 2000 25:247-251
14891	27-28	putative protein contains PFAM 02536 mTERF (mitochondrial transcription termination factor) domain; large gene family in <i>Arabidopsis</i> of unknown function proteins	Fernandez-Silva, P. <i>et al.</i> (1997) EMBO J 16:1066-1079
14986	29-30	ubiquitin isopeptidase T (aka ubiquitin-specific protease 14)	Wilkinson, K.D. <i>et al.</i> (1995) Biochemistry 34:14535- 14546; Falquet, L. <i>et al.</i> (1995) FEBS Lett 376:233- 237; Lindsey, D.F. <i>et al.</i> (1998) J Biol Chem 273:29178-29187
15377	31-32	putative formyl transferase similar to <i>B. napus</i> methionyl tRNA transformylase Fmt protein (AJ245479) & <i>B. rapa</i> S-locus protein 8 (AB022076)	Cui Y <i>et al.</i> (1999) Plant Cell. 11:2217-2231; Suzuki, G. <i>et</i> <i>al.</i> (1999) Genetics 153:391- 400; Cusack S. (1999) Curr Opin Struct Biol. 9:66-73
16219	33-34	polyadenylation cleavage/specificity factor 100 kDa subunit (AF283277)	Bilger, A. <i>et al.</i> (1994) Genes Dev. 8:1106-1116; Bienroth, S. <i>et al.</i> (1993) EMBO J. 12:585-594; Jenny, A. <i>et al.</i> (1994) Mol Cell Biol. 14:8183-8190
16547	35-36	similarity to UV-induced protein Uvi31, <i>S. pombe</i> , G1381578 unknown function, but similar to Pectobacterium chrysanthemi SufE protein (AJ301654) involved in iron metabolism, <i>S. pombe</i> uvi31 protein of the BolA / YRBA family (Q12238), Synechocystis hypothetical 17.7 KDA protein SLR1419 (P74523)	Kim, S.H. <i>et al.</i> (1997) Environ Mol Mutagen 30:72- 81; Santos, J.M. <i>et al.</i> (1999) Mol Microbiol 32:789-798

20933	37-38	hypothetical protein contains WD40 repeats, similar to human CIAO 1 gene (O76071) & <i>S. cerevisiae</i> YDR267c (S70127)	Neer, E.J. <i>et al.</i> (1994) <i>Nature</i> 371:297-300; Johnstone, R.W. <i>et al.</i> (1998) <i>J Biol Chem</i> 273:10880-10887
21455	39-40	putative protein small gene family in <i>Arabidopsis</i> of unknown function proteins	none
21878	41-42	<i>Arabidopsis</i> digalactosyldiacylglycerol synthase (DGD1, AAD42378)	Dormann, P. <i>et al.</i> (1999) <i>Science</i> 284:2181-2184; Hartel, H. <i>et al.</i> (1997) <i>Plant Physiol</i> 115:1175-1184
23915	43-44	hypothetical protein contains PPR motifs, member of large gene family in <i>Arabidopsis</i>	Small, I.D. & Peeters, N. (2000) <i>Trends Biochem Sci</i> 25:46-47; Manthey, G.M. & McEwen, J.E. (1995) <i>EMBO J</i> 14:4031-4043; Barkan, A. <i>et al.</i> (1994) <i>EMBO J</i> 13:3170- 3181
30945	45-46	unknown protein similar to rice hypothetical protein (BAB56056)	none
31895	47-48	similar to unknown protein small gene family in <i>Arabidopsis</i> of unknown function proteins	none
34269	49-50	unknown protein	none
34540	51-52	probable lipoate protein ligase B, similar to <i>Mycobacterium</i> LIPB gene (O32961) also similar to <i>S. pombe</i> putative pre-tRNA/pre-rRNA processing protein (T41635)	Reed, K.E. & Cronan, J.E. Jr. (1993) <i>J Bacteriol</i> 175:1325- 1336; Chen, X.J. (1997) <i>Mol. Gen. Genet.</i> 255:341-349
34555	53-54	similar to <i>Synechocystis</i> hypothetical 41.9KD protein (P52640) similar to several prokaryotic proteins of unknown function including <i>E. coli</i> YJEQ (P39286)	none
35154	55-56	similar to unknown protein similar to human hypothetical protein (BAA91556), <i>S. cerevisiae</i> probable membrane protein YOR262w (S67159), & <i>S. pombe</i> ATP(GTP)-binding protein Fet5 (AAC49837)	Shpakovskii, G.V. & Lebedenko, E.N. (1997) <i>Bioorg. Khim.</i> 23:234-237
35438	57-58	unknown protein weak similarity to <i>Pennisetum ciliare</i> unknown function protein (AAK15504)	none

37351	59-60	strong similarity to obtusifoliol 14-alpha demethylase (CYP51; P93846) from Sorghum bicolor (also wheat & rice), member of the PFL00067 cytochrome P450 family	Kushiro, M. <i>et al.</i> (2001) Biochem Biophys Res Commun. 285:98-104; Bak <i>et al.</i> (1997) Plant J. 11:191-201; Grausem, B. (1995) Plant J. 7:761-770
37389	61-62	similar to human GLE1-like required for poly(A)+ RNA export (AAC25561)	Watkins, J.L. <i>et al.</i> (1998) Proc. Natl. Acad. Sci. U.S.A. 95:6779-6784; Murphy, R. & Wente, S.R. (1996) Nature 383:357-360
38108	63-64	<i>Arabidopsis</i> 4-(cytidine 5'-phospho)-2-C-methyl-D-erythritol kinase (aka ispE & 4-diphosphocytidyl-2-C-methyl-Derythritol kinase) (AF288615) similar to <i>E. coli</i> ychB (aka ispE) gene (P24209)	Rohdich, F. <i>et al.</i> (2000) Proc Natl Acad Sci U.S.A. 97:8251-8256; Luettgen, H. <i>et al.</i> (2000) Proc. Natl. Acad. Sci. U.S.A. 97:1062-1067; Lange, B.M. & Croteau, R. (1999) Proc Natl Acad Sci U.S.A. 96:13714-13719
43301	65-66	similar to hypothetical bacterial proteins, including <i>Pseudomonas aeruginosa</i> protein PA0292 (F83608) & <i>Lactococcus lactis</i> (AAK05795)	none
46250	67-68	hypothetical protein weak similarity to hypothetical proteins from <i>Arabidopsis</i> (AAG51506) and mouse (BAB23375)	none
47050A	69-70	unknown protein weak similarity to <i>Botrytis</i> cDNA (AL115827)	none
52949A	71-72	6-phosphogluconolactonase-like protein similar to 6-phosphogluconolactonases such as human (O95336), <i>Brassica carinata</i> (AAK50346), & <i>Mycobacterium tuberculosis</i> (devB, CAB09261)	Collard, F. <i>et al.</i> (1999) FEBS Lett. 459:223-226; Bauer, H.P. <i>et al.</i> (1983) Eur J Biochem. 133:163-168
53210A	73-74	putative heat shock protein in hsp90 family similar to rye hsp82 (S65776), <i>Ipomoea nil</i> hsp83 (P51819), chicken hsp90 beta (Q04619) and others	Felsheim, R.F. & Das, A. (1992) Plant Physiol. 100:1764-1771; Coates, A.R. <i>et al.</i> (1999) <i>Biotechnol Genet Eng Rev</i> 16:393-405; Milioni, D. & Hatzopoulos, P. (1997) <i>Plant Mol Biol</i> 35:955-961

55483	75-76	putative para-aminobenzoate synthase and glutamine amidotransferase, a bifunctional enzyme similar to <i>Streptomyces pristinaespiralis</i> papA (AAC44866), <i>E. coli</i> pabB (P05041) & pabA (P00903), and <i>Bacillus stearothermophilus</i> anthranilate synthase component I trpE (AAD33791)	Goncharoff, P. & Nichols, B.P. (1984) <i>J Bacteriol.</i> 159:57-62.; Roux, B. & Walsh, C.T. (1992) <i>Biochemistry.</i> 31:6904-6910; Kaplan, J.B. & Nichols, B.P. (1983) <i>J Mol Biol</i> 168:451-468
58351A	77-78	26S proteasome p55 protein-like similar to human 26S proteasome regulatory complex chain p55 (BAA19749), <i>S. cerevisiae</i> 26S proteasome regulatory complex chain RPN5 (S67695), and others	Saito, A. <i>et al.</i> (1997) <i>Gene</i> 203:241-250; Glickman, M.H. <i>et al.</i> (1998) <i>Mol Cell Biol</i> 18:3149-3162
60944	79-80	similar to <i>Guillardia theta</i> chloroplast 50S ribosomal protein L31 (O46917)	Yamaguchi, K. & Subramanian, A.R. (2000) <i>J Biol Chem.</i> 275:28466-28482
62837	81-82	AtClpC: regulatory subunit of Clp protease with ATPase activity (BAA82062)	Adam, Z. (2000) <i>Biochimie</i> 82:647-654; Sokolenko, A. <i>et al.</i> (1998) <i>Planta</i> 207:286-295; Nakabayashi, K. <i>et al.</i> (1999) <i>Plant Cell Physiol.</i> 40:504-514; Maurizi, M.R. <i>et al.</i> (1990) <i>J Biol Chem.</i> 265:12536-12545
65310	83-84	26S proteasome regulatory subunit S3, contains a PCI PF01399 domain similar to 26S proteasome regulatory subunit S3 from <i>Nicotiana tabacum</i> (P93768), carrot (Q06364), human (O43242), <i>S. cerevisiae</i> RPN3 (P40016), and others	Voges, D. <i>et al.</i> (1999) <i>Ann Rev Biochem</i> 68:1015-1068; Fu, H. <i>et al.</i> (1999) <i>Mol Biol Rep</i> 26:137-146; Fu, H. <i>et al.</i> (1999) <i>Plant J</i> 18:529-539; Kominami, K. <i>et al.</i> (1997) <i>Mol Biol Cell</i> 8:171-187
68181	85-86	small zinc finger-like protein TIM9 similar to mitochondrial import inner membrane translocase subunit TIM9 from several plants and <i>S. cerevisiae</i> (O74700)	Koehler, C.M. <i>et al.</i> (1998) <i>EMBO J.</i> 17:6477-6486; Tokatlidis, K. <i>et al.</i> (2000) <i>Biochem Soc Trans</i> 28:495-499
70913	87-88	<i>Arabidopsis</i> CCAAT binding protein/transcription factor Hap2a (CAA74048)	Edwards, D. <i>et al.</i> (1998) <i>Plant Physiol</i> 117:1015-1022; Albani, D. & Robert, L.S. (1995) <i>Gene</i> 167:209-213

71067	89-90	hypothetical protein gene family in <i>Arabidopsis</i> of unknown function proteins	none
71654	91-92	poly(A) binding protein-like	Hilson, P. <i>et al.</i> (1993) <i>Plant Physiol</i> 103:525-533; Belostotsky, D.A. & Meagher, R.B. (1993) <i>Proc Natl Acad Sci U.S.A.</i> 90:6686-6690; Gallie, D.R. (1998) <i>Gene</i> 216:1-11
ET3172	93-94	hypothetical protein small gene family in <i>Arabidopsis</i> (T47999 & T02193) of unknown function	none
ET3546	95-96	cdc27/nuc2-like protein, may contain TPR-repeat similar to human cdc27 (P30260), <i>S. pombe</i> nuc2 (P10505), <i>S. cerevisiae</i> cdc23 (P16522), and others	Hirano, T. <i>et al.</i> (1988) <i>J. Cell Biol.</i> 106:1171-1183; Chen, P.L. <i>et al</i> (1995) <i>Cell Growth Differ.</i> 6:199-210

Example 10: Expression of Recombinant Essential Proteins in *E. coli*

The coding region of each of the essential proteins, corresponding to cDNA clones of odd-numbered SEQ ID NO:1-96, is subcloned into an appropriate expression vector, and transformed into *E. coli* using the manufacturer's conditions. Specific examples include plasmids such as pBluescript (Stratagene, La Jolla, CA), pFLAG (International Biotechnologies, Inc., New Haven, CT), and pTrcHis (Invitrogen, La Jolla, CA). *E. coli* is cultured, and expression of the essential protein is confirmed. Recombinant protein is isolated using standard techniques.

Example 11: *In Vitro* Binding Assays

Recombinant protein for each of the essential genes described in this application is obtained, for example, according to Example 10. The protein is immobilized on chips appropriate for ligand binding assays using techniques that are well known in the art. The protein immobilized on the chip is exposed to sample compound in solution according to methods well known in the art. While the sample compound is in contact with the immobilized protein, measurements capable of detecting protein-ligand interactions are conducted. Examples of such measurements are SELDI, biacore and FCS, described above. Compounds

found to bind the protein are readily discovered in this fashion and are subjected to further characterization.

The above-disclosed embodiments are illustrative. This disclosure of the invention
5 will place one skilled in the art in possession of many variations of the invention. All such
obvious and foreseeable variations are intended to be encompassed by the present invention.

CLAIMS:

1. A method of identifying a herbicidal compound, comprising:
 - a) combining a polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOS:2-96 with a compound to be tested for the ability to bind to said polypeptide, under conditions conducive to binding;
 - b) selecting a compound identified in (a) that binds to said polypeptide;
 - c) applying a compound selected in (b) to a plant to test for herbicidal activity; and
 - d) selecting a compound identified in (c) that has herbicidal activity.
2. The method according to claim 1, wherein said polypeptide comprises an amino acid sequence at least 95% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOS:2-96.
3. The method according to claim 2, wherein said polypeptide comprises an amino acid sequence at least 99% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOS:2-96.
4. The method according to claim 3, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOS:2-96.
5. A method of identifying a herbicidal compound, comprising:
 - c) combining a polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOS:2-96 with a compound to be tested for the ability to inhibit the activity of said polypeptide, under conditions conducive to inhibition;
 - d) selecting a compound identified in (a) that inhibits the activity of said polypeptide;
 - c) applying a compound selected in (b) to a plant to test for herbicidal activity; and
 - d) selecting a compound identified in (c) that has herbicidal activity.

6. The method according to claim 5, wherein said polypeptide comprises an amino acid sequence at least 95% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.

5 7. The method according to claim 6, wherein said polypeptide comprises an amino acid sequence at least 99% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.

10 8. The method according to claim 7, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.

9. A method for killing or inhibiting the growth or viability of a plant, comprising applying to the plant a herbicidal compound identified according to the method of claim 1.

15 10. A method for killing or inhibiting the growth or viability of a plant, comprising applying to the plant a herbicidal compound identified according to the method of claim 5.

SEQUENCE LISTING

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His Ser Leu Lys His Leu Cys Ala Ala Met Val Pro Val Phe Leu Thr
225 230 235 240

ctc atg ctt gcg aaa aga acc gtt caa act gag agg att agc ttg tat 768
 Leu Met Leu Ala Lys Arg Thr Val Gln Thr Glu Arg Ile Ser Leu Tyr
 245 250 255

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Lys Thr Trp Lys Lys Gly Ser Glu Glu Glu Arg Phe Glu His Ser Tyr
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35 40 45

Asn Val Ile Ser Asn Phe Pro Phe Leu Ile Ile Gly Phe Ile Gly Leu
50 55 60

Ile Leu Cys Phe Tyr Pro Glu Asp Tyr Phe Ser Phe Ser Leu Arg Gly
65 70 75 80

Glu Lys Ile Gly Trp Thr Cys Phe Tyr Ile Gly Val Ala Ala Val Ala
85 90 95

Phe Gly Ser Ser Tyr Tyr His Leu His Pro Asn Asp Ala Thr Leu Leu
 100 105 110

Trp Asp Arg Leu Pro Met Thr Ile Ala Phe Thr Ser Ile Met Ala Ile
 115 120 125

Phe Val Ile Glu Arg Ile Asp Glu His Lys Gly Thr Tyr Ser Ile Ala
 130 135 140

Pro Leu Leu Leu Ala Gly Leu Val Ser Ile Leu Tyr Trp Arg Phe Phe
145 150 155 160

Asp Asp Leu Arg Pro Tyr Ala Leu Val Gln Phe Val Pro Cys Ile Val
165 170 175

Ile Pro Leu Met Ala Ile Leu Leu Pro Pro Met Tyr Thr His Ser Thr
180 185 190

Tyr Trp Leu Trp Ala Ala Gly Phe Tyr Leu Leu Ala Lys Val Glu Glu
195 200 205

Ala Ala Asp Lys Pro Ile Tyr Ser Trp Thr His His Ile Ile Ser Gly
210 215 220

His Ser Leu Lys His Leu Cys Ala Ala Met Val Pro Val Phe Leu Thr
225 230 235 240

.

Leu Met Leu Ala Lys Arg Thr Val Gln Thr Glu Arg Ile Ser Leu Tyr
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Ser Asn Val Ala Val Glu Glu Thr Arg
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act cag ttg ttg aaa aga tca aaa agt ttt ggt ctt gtt cggttt ccc			96
Thr Gln Leu Leu Lys Arg Ser Lys Ser Phe Gly Leu Val Arg Phe Pro			
20	25	30	
gcc aag tat gga ctg gga gct acc cggttt cca gtc			144
Ala Lys Tyr Gly Leu Gly Ala Thr Arg Lys Lys Gln Leu Phe Arg Val			
35	40	45	
tat gcg tct gaa agt agt agt ggg tct tca tct aat agc gat gga ggc			192
Tyr Ala Ser Glu Ser Ser Gly Ser Ser Ser Asn Ser Asp Gly Gly			
50	55	60	
ttt tcg tgg gtg aga ttg gct cag tct att cgc ctt ggt gcc gag cggttt			240
Phe Ser Trp Val Arg Leu Ala Gln Ser Ile Arg Leu Gly Ala Glu Arg			
65	70	75	80
att ggg gag aag att gga gaa tct gtg aag aca gaa att ggg ttt gac			288
Ile Gly Glu Lys Ile Gly Glu Ser Val Lys Thr Glu Ile Gly Phe Asp			
85	90	95	
tcg gaa gaa gca agt ggg aga gtg aat gag tat gtg gct cga gtt aag			336
Ser Glu Glu Ala Ser Gly Arg Val Asn Glu Tyr Val Ala Arg Val Lys			
100	105	110	
gat agt gtg cac aag ggc cat cac gag ctg act cgc ttt aag aat gag			384
Asp Ser Val His Lys Gly His His Glu Leu Thr Arg Phe Lys Asn Glu			
115	120	125	
aca gtg cct tcg ttt att gat tgg aac aag tgg gag cat tgg aag gac			432
Thr Val Pro Ser Phe Ile Asp Trp Asn Lys Trp Glu His Trp Lys Asp			
130	135	140	
atc agg aat tgg gac ggt aaa cga gtt gct gcc ttg ttc ata tat gct			480
Ile Arg Asn Trp Asp Gly Lys Arg Val Ala Ala Leu Phe Ile Tyr Ala			
145	150	155	160
ttt gcg ctg tta ctt tct tgt caa aga gtt tat gtt gcc atc caa gct			528
Phe Ala Leu Leu Ser Cys Gln Arg Val Tyr Val Ala Ile Gln Ala			
165	170	175	
cct cgg gta gaa cga gag aga aga gag tta aca gag tct ttt atg gag			576
Pro Arg Val Glu Arg Glu Arg Arg Glu Leu Thr Glu Ser Phe Met Glu			
180	185	190	
gct ttg atc ccc gag cca tct cct gga aat ata gaa aag ttc aag aga			624
Ala Leu Ile Pro Glu Pro Ser Pro Gly Asn Ile Glu Lys Phe Lys Arg			
195	200	205	
aat atg tgg agg aaa gca aca cct aaa ggc ttg aaa tta aaa agg ttc			672
Asn Met Trp Arg Lys Ala Thr Pro Lys Gly Leu Lys Leu Lys Arg Phe			
210	215	220	
att gaa gcg cct gat gga aca ctt gtc cac gat agt tct tat gtt gga			720
Ile Glu Ala Pro Asp Gly Thr Leu Val His Asp Ser Ser Tyr Val Gly			
225	230	235	240
gaa aat gcg tgg gat gac gat cta gag acc aca gag gga tct ctc aag			768

Glu Asn Ala Trp Asp Asp Asp Leu Glu Thr Thr Glu Gly Ser Leu Lys			
245	250	255	
aaa ata att ggt aga aat gct agg att cag aca gag gca aag aag aaa			816
Lys Ile Ile Gly Arg Asn Ala Arg Ile Gln Thr Glu Ala Lys Lys Lys			
260	265	270	
ctc agc caa gat ctg ggt gtc tct ggt gaa att gga gac agt gta ggt			864
Leu Ser Gln Asp Leu Gly Val Ser Gly Glu Ile Gly Asp Ser Val Gly			
275	280	285	
aat tgg cgg gaa agg ctt gca acc tgg aag gaa atg tta gaa cga gaa			912
Asn Trp Arg Glu Arg Leu Ala Thr Trp Lys Glu Met Leu Glu Arg Glu			
290	295	300	
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Lys Leu Ser Glu Gln Leu Asn Ser Ser Ala Ala Lys Tyr Val Val Glu			
305	310	315	320
ttt gat atg aaa gag gta gag aaa agt ctt cgc gaa gat gtt att gga			1008
Phe Asp Met Lys Glu Val Glu Lys Ser Leu Arg Glu Asp Val Ile Gly			
325	330	335	
agg aca tct gaa act gag gga act aga gct ctc tgg ata tca aag aga			1056
Arg Thr Ser Glu Thr Glu Gly Thr Arg Ala Leu Trp Ile Ser Lys Arg			
340	345	350	
tgg tgg cga tat cgc cct aag ctt ccc tat acc tac ttc ctt cag aag			1104
Trp Trp Arg Tyr Arg Pro Lys Leu Pro Tyr Thr Phe Leu Gln Lys			
355	360	365	
ctt gat tct tct gag gtt gca gct gtt gtt ttc acg gaa gac cta aag			1152
Leu Asp Ser Ser Glu Val Ala Ala Val Val Phe Thr Glu Asp Leu Lys			
370	375	380	
aga ttg tat gtg acc atg aaa gaa ggt ttc cct cta gaa tat att gtt			1200
Arg Leu Tyr Val Thr Met Lys Glu Gly Phe Pro Leu Glu Tyr Ile Val			
385	390	395	400
gac att ccc tta gat cct tac ttg ttt gag act att tgc aac gcc gga			1248
Asp Ile Pro Leu Asp Pro Tyr Leu Phe Glu Thr Ile Cys Asn Ala Gly			
405	410	415	
gtt gag gtg gat ctt ctt cag aag agg cag atc cac tac ttc atg aaa			1296
Val Glu Val Asp Leu Leu Gln Lys Arg Gln Ile His Tyr Phe Met Lys			
420	425	430	
gtt ttc att gca ctt ctg ccg ggg ata cta att tta tgg ttt ata aga			1344
Val Phe Ile Ala Leu Leu Pro Gly Ile Leu Ile Leu Trp Phe Ile Arg			
435	440	445	
gaa tct gcc atg ctt ctc ctt atc aca tcc aag cgc ttt ctc tac aag			1392
Glu Ser Ala Met Leu Leu Ile Thr Ser Lys Arg Phe Leu Tyr Lys			
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aag tat aat cag ctg ttt gat atg gct tat gca gaa aat ttt ata ttg			1440
Lys Tyr Asn Gln Leu Phe Asp Met Ala Tyr Ala Glu Asn Phe Ile Leu			
465	470	475	480
ccg gtt gga gat gtc agt gag aca aaa tca atg tat aag gaa gtg gta			1488

Pro Val Gly Asp Val Ser Glu Thr Lys Ser Met Tyr Lys Glu Val Val			
485	490	495	
cta ggc ggt gat gtc tgg gat ctt ctt gat gag cta atg atc tac atg			1536
Leu Gly Gly Asp Val Trp Asp Leu Leu Asp Glu Leu Met Ile Tyr Met			
500	505	510	
ggg aac cca atg caa tac tat gaa aaa gat gtg gct ttt gtc agg ggt			1584
Gly Asn Pro Met Gln Tyr Tyr Glu Lys Asp Val Ala Phe Val Arg Gly			
515	520	525	
gtg ctt ctt tct gga cct cct gga act gga aaa aca ctt ttt gcg cga			1632
Val Leu Leu Ser Gly Pro Pro Gly Thr Gly Lys Thr Leu Phe Ala Arg			
530	535	540	
aca ctt gca aag gaa agt ggg cta cca ttt gtg ttt gca tct ggt gcg			1680
Thr Leu Ala Lys Glu Ser Gly Leu Pro Phe Val Phe Ala Ser Gly Ala			
545	550	555	560
gag ttc aca gac agt gaa aaa agt ggt gct gca aag atc aat gag atg			1728
Glu Phe Thr Asp Ser Glu Lys Ser Gly Ala Ala Lys Ile Asn Glu Met			
565	570	575	
ttt tca atc gcg aga cga aat gcc cct gct ttt gtg ttt gtg gat gaa			1776
Phe Ser Ile Ala Arg Arg Asn Ala Pro Ala Phe Val Phe Val Asp Glu			
580	585	590	
ata gat gct att gct ggt aga cat gct aga aaa gat cca cgg aga aga			1824
Ile Asp Ala Ile Ala Gly Arg His Ala Arg Lys Asp Pro Arg Arg Arg			
595	600	605	
gca act ttt gaa gct tta att gcg caa ctc gat ggg gag aaa gag aag			1872
Ala Thr Phe Glu Ala Leu Ile Ala Gln Leu Asp Gly Glu Lys Glu Lys			
610	615	620	
aca ggt atc gat agg ttt tct ttg aga caa gct gtg ata ttt atc tgt			1920
Thr Gly Ile Asp Arg Phe Ser Leu Arg Gln Ala Val Ile Phe Ile Cys			
625	630	635	640
gct acc aat aga cct gat gaa ctc gac ctt gag ttt gtc cgt tct ggc			1968
Ala Thr Asn Arg Pro Asp Glu Leu Asp Leu Glu Phe Val Arg Ser Gly			
645	650	655	
cgt att gac cgt cgg ctg tat att ggg ttg cct gat gca aag caa agg			2016
Arg Ile Asp Arg Arg Leu Tyr Ile Gly Leu Pro Asp Ala Lys Gln Arg			
660	665	670	
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Val Gln Ile Phe Gly Val His Ser Ala Gly Lys Asn Leu Ala Glu Asp			
675	680	685	
ata gac ttt ggg aag ctt gtt ttt cga acg gtt ggc ttt tcc ggg gca			2112
Ile Asp Phe Gly Lys Leu Val Phe Arg Thr Val Gly Phe Ser Gly Ala			
690	695	700	
gat atc cgg aat ctt gtt aac gaa gcg gct ata atg tcg gta agg aag			2160
Asp Ile Arg Asn Leu Val Asn Glu Ala Ala Ile Met Ser Val Arg Lys			
705	710	715	720
gga cgt tct tac ata tat caa caa gac att gtt gat gtg tta gat aaa			2208

Gly Arg Ser Tyr Ile Tyr Gln Gln Asp Ile Val Asp Val Leu Asp Lys			
725	730	735	
caa ttg ctc gag ggt atg ggt gta ctt ctt aca gag gaa gag caa cag			2256
Gln Leu Leu Glu Gly Met Gly Val Leu Leu Thr Glu Glu Gln Gln			
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Lys Cys Glu Gln Ser Val Ser Tyr Glu Lys Lys Arg Leu Leu Ala Val			
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cat gag gct ggt cat ata gtg ttg gct cat ttg ttt cct cga ttt gac			2352
His Glu Ala Gly His Ile Val Leu Ala His Leu Phe Pro Arg Phe Asp			
770	775	780	
tgg cat gca ttt tcg cag ctc ctt cct ggt ggc aag gaa act gct gta			2400
Trp His Ala Phe Ser Gln Leu Leu Pro Gly Gly Lys Glu Thr Ala Val			
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Ser Val Phe Tyr Pro Arg Glu Asp Met Val Asp Gln Gly Tyr Thr Thr			
805	810	815	
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Phe Gly Tyr Met Lys Met Gln Met Val Val Ala His Gly Gly Arg Cys			
820	825	830	
gct gaa cgt gtg gtt ttt ggc gat aat gtc act gat gga gga aaa gat			2544
Ala Glu Arg Val Val Phe Gly Asp Asn Val Thr Asp Gly Gly Lys Asp			
835	840	845	
gac ctg gag aag ata aca aaa att gcc agg gag atg gtg att agc cct			2592
Asp Leu Glu Lys Ile Thr Lys Ile Ala Arg Glu Met Val Ile Ser Pro			
850	855	860	
caa agt gcg aga tta ggt ctc act caa ctt gta aaa aag att gga atg			2640
Gln Ser Ala Arg Leu Gly Leu Thr Gln Leu Val Lys Lys Ile Gly Met			
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gtg gat tta cca gat aac cca gac ggc gag ctg ata aaa tac cgg tgg			2688
Val Asp Leu Pro Asp Asn Pro Asp Gly Glu Leu Ile Lys Tyr Arg Trp			
885	890	895	
gac cat cct cat gta atg cca gca gag atg tcg gta gaa gta tcc gag			2736
Asp His Pro His Val Met Pro Ala Glu Met Ser Val Glu Val Ser Glu			
900	905	910	
cta ttc acc cgt gag ttg aca agg tat atc gag gag act gaa gaa ctt			2784
Leu Phe Thr Arg Glu Leu Thr Arg Tyr Ile Glu Glu Thr Glu Glu Leu			
915	920	925	
gcg atg aat gct ctg aga gca aac agg cac att ctg gac tta atc acc			2832
Ala Met Asn Ala Leu Arg Ala Asn Arg His Ile Leu Asp Leu Ile Thr			
930	935	940	
aga gag tta tta gaa aaa tca agg att act gga ttg gaa gtg gaa gag			2880
Arg Glu Leu Leu Glu Lys Ser Arg Ile Thr Gly Leu Glu Val Glu Glu			
945	950	955	960
aaa atg aag gat ctt tct ccg tta atg ttt gag gat ttt gtg aag cca			2928

Lys	Met	Lys	Asp	Leu	Ser	Pro	Leu	Met	Phe	Glu	Asp	Phe	Val	Lys	Pro
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Phe	Gln	Ile	Asn	Pro	Asp	Asp	Glu	Glu	Leu	Leu	Pro	His	Lys	Asp	Arg
980								985					990		
gtg agc tat cag cca gtt gat tta cgt gct gcg cca ctc cac aga agc															3024
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20							25					30			
Ala Lys Tyr Gly Leu Gly Ala Thr Arg Lys Lys Gln Leu Phe Arg Val															
35							40					45			
Tyr Ala Ser Glu Ser Ser Gly Ser Ser Ser Asn Ser Asp Gly Gly															
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Phe Ser Trp Val Arg Leu Ala Gln Ser Ile Arg Leu Gly Ala Glu Arg															
65							70					75			80
Ile Gly Glu Lys Ile Gly Glu Ser Val Lys Thr Glu Ile Gly Phe Asp															
85							90					95			
Ser Glu Glu Ala Ser Gly Arg Val Asn Glu Tyr Val Ala Arg Val Lys															
100							105					110			
Asp Ser Val His Lys Gly His His Glu Leu Thr Arg Phe Lys Asn Glu															
115							120					125			
Thr Val Pro Ser Phe Ile Asp Trp Asn Lys Trp Glu His Trp Lys Asp															
130							135					140			

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145 150 155 160

Phe Ala Leu Leu Leu Ser Cys Gln Arg Val Tyr Val Ala Ile Gln Ala
165 170 175

Pro Arg Val Glu Arg Glu Arg Arg Glu Leu Thr Glu Ser Phe Met Glu
180 185 190

Ala Leu Ile Pro Glu Pro Ser Pro Gly Asn Ile Glu Lys Phe Lys Arg
195 200 205

Asn Met Trp Arg Lys Ala Thr Pro Lys Gly Leu Lys Leu Lys Arg Phe
210 215 220

Ile Glu Ala Pro Asp Gly Thr Leu Val His Asp Ser Ser Tyr Val Gly
225 230 235 240

Glu Asn Ala Trp Asp Asp Asp Leu Glu Thr Thr Glu Gly Ser Leu Lys
245 250 255

Lys Ile Ile Gly Arg Asn Ala Arg Ile Gln Thr Glu Ala Lys Lys Lys
260 265 270

Leu Ser Gln Asp Leu Gly Val Ser Gly Glu Ile Gly Asp Ser Val Gly
275 280 285

Asn Trp Arg Glu Arg Leu Ala Thr Trp Lys Glu Met Leu Glu Arg Glu
290 295 300

Lys Leu Ser Glu Gln Leu Asn Ser Ser Ala Ala Lys Tyr Val Val Glu
305 310 315 320

Phe Asp Met Lys Glu Val Glu Lys Ser Leu Arg Glu Asp Val Ile Gly
325 330 335

Arg Thr Ser Glu Thr Glu Gly Thr Arg Ala Leu Trp Ile Ser Lys Arg
340 345 350

Trp Trp Arg Tyr Arg Pro Lys Leu Pro Tyr Thr Tyr Phe Leu Gln Lys
355 360 365

Leu Asp Ser Ser Glu Val Ala Ala Val Val Phe Thr Glu Asp Leu Lys
370 375 380

Arg Leu Tyr Val Thr Met Lys Glu Gly Phe Pro Leu Glu Tyr Ile Val
385 390 395 400

Asp Ile Pro Leu Asp Pro Tyr Leu Phe Glu Thr Ile Cys Asn Ala Gly
405 410 415

Val Glu Val Asp Leu Leu Gln Lys Arg Gln Ile His Tyr Phe Met Lys
420 425 430

Val Phe Ile Ala Leu Leu Pro Gly Ile Leu Ile Leu Trp Phe Ile Arg
435 440 445

Glu Ser Ala Met Leu Leu Leu Ile Thr Ser Lys Arg Phe Leu Tyr Lys
450 455 460

Lys Tyr Asn Gln Leu Phe Asp Met Ala Tyr Ala Glu Asn Phe Ile Leu
465 470 475 480

Pro Val Gly Asp Val Ser Glu Thr Lys Ser Met Tyr Lys Glu Val Val
485 490 495

Leu Gly Gly Asp Val Trp Asp Leu Leu Asp Glu Leu Met Ile Tyr Met
500 505 510

Gly Asn Pro Met Gln Tyr Tyr Glu Lys Asp Val Ala Phe Val Arg Gly
515 520 525

Val Leu Leu Ser Gly Pro Pro Gly Thr Gly Lys Thr Leu Phe Ala Arg
530 535 540

Thr Leu Ala Lys Glu Ser Gly Leu Pro Phe Val Phe Ala Ser Gly Ala
545 550 555 560

Glu Phe Thr Asp Ser Glu Lys Ser Gly Ala Ala Lys Ile Asn Glu Met
565 570 575

Phe Ser Ile Ala Arg Arg Asn Ala Pro Ala Phe Val Phe Val Asp Glu
580 585 590

Ile Asp Ala Ile Ala Gly Arg His Ala Arg Lys Asp Pro Arg Arg Arg
595 600 605

Ala Thr Phe Glu Ala Leu Ile Ala Gln Leu Asp Gly Glu Lys Glu Lys
610 615 620

Thr Gly Ile Asp Arg Phe Ser Leu Arg Gln Ala Val Ile Phe Ile Cys
625 630 635 640

Ala Thr Asn Arg Pro Asp Glu Leu Asp Leu Glu Phe Val Arg Ser Gly
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Arg Ile Asp Arg Arg Leu Tyr Ile Gly Leu Pro Asp Ala Lys Gln Arg
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Val Gln Ile Phe Gly Val His Ser Ala Gly Lys Asn Leu Ala Glu Asp
675 680 685

Ile Asp Phe Gly Lys Leu Val Phe Arg Thr Val Gly Phe Ser Gly Ala
690 695 700

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Gly Arg Ser Tyr Ile Tyr Gln Gln Asp Ile Val Asp Val Leu Asp Lys
725 730 735

Gln Leu Leu Glu Gly Met Gly Val Leu Leu Thr Glu Glu Gln Gln
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Lys Cys Glu Gln Ser Val Ser Tyr Glu Lys Lys Arg Leu Leu Ala Val
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His Glu Ala Gly His Ile Val Leu Ala His Leu Phe Pro Arg Phe Asp
770 775 780

Trp His Ala Phe Ser Gln Leu Leu Pro Gly Gly Lys Glu Thr Ala Val
785 790 795 800

Ser Val Phe Tyr Pro Arg Glu Asp Met Val Asp Gln Gly Tyr Thr Thr
805 810 815

Phe Gly Tyr Met Lys Met Gln Met Val Val Ala His Gly Gly Arg Cys
820 825 830

Ala Glu Arg Val Val Phe Gly Asp Asn Val Thr Asp Gly Gly Lys Asp
835 840 845

Asp Leu Glu Lys Ile Thr Lys Ile Ala Arg Glu Met Val Ile Ser Pro
850 855 860

Gln Ser Ala Arg Leu Gly Leu Thr Gln Leu Val Lys Lys Ile Gly Met
865 870 875 880

Val Asp Leu Pro Asp Asn Pro Asp Gly Glu Leu Ile Lys Tyr Arg Trp
885 890 895

Asp His Pro His Val Met Pro Ala Glu Met Ser Val Glu Val Ser Glu
900 905 910

Leu Phe Thr Arg Glu Leu Thr Arg Tyr Ile Glu Glu Thr Glu Glu Leu
915 920 925

Ala Met Asn Ala Leu Arg Ala Asn Arg His Ile Leu Asp Leu Ile Thr
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Arg Glu Leu Leu Glu Lys Ser Arg Ile Thr Gly Leu Glu Val Glu Glu
945 950 955 960

Lys Met Lys Asp Leu Ser Pro Leu Met Phe Glu Asp Phe Val Lys Pro
965 970 975

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Cys Asp Phe Ser Ser Ser Phe Ser Leu Ala Ser Ser Ser Ser Ser Thr			
20	25	30	
gtc tcc gtc aca acc ttc aac att tcc tct ctt tcc tct aac ccc aac			144
Val Ser Val Thr Thr Phe Asn Ile Ser Ser Leu Ser Ser Asn Pro Asn			
35	40	45	
atc atc aat tcc agc tca act ctc ttc cgt tcc ctt tcc ttc tcc ctt			192
Ile Ile Asn Ser Ser Ser Thr Leu Phe Arg Ser Leu Ser Phe Ser Leu			
50	55	60	
atc cgc cac cgc agc agc tac tca cgt cgc tct ctc cgc cgt ctc tct			240
Ile Arg His Arg Ser Ser Tyr Ser Arg Arg Ser Leu Arg Arg Leu Ser			
65	70	75	80
atc cac aca gtt cat gga aac aaa acc caa ttc ttc tct cac tcg tct			288
Ile His Thr Val His Gly Asn Lys Thr Gln Phe Phe Ser His Ser Ser			
85	90	95	
aca cga act cca cca ctt ttc acg gct aat tcc aca gcc caa cga agc			336
Thr Arg Thr Pro Pro Leu Phe Thr Ala Asn Ser Thr Ala Gln Arg Ser			
100	105	110	
ggg act ttc gtc gaa cac ctt aca ggc att aca gaa tcg gaa gaa gga			384
Gly Thr Phe Val Glu His Leu Thr Gly Ile Thr Glu Ser Glu Glu Gly			
115	120	125	
atc agc gaa gcc aac ggt ttc ggt gat gta gag tct gct agg aac gac			432
Ile Ser Glu Ala Asn Gly Phe Gly Asp Val Glu Ser Ala Arg Asn Asp			
130	135	140	
ata aga aac gtc gcg act cgt aga ata gag acg gag ttt gaa gtt aga			480
Ile Arg Asn Val Ala Thr Arg Arg Ile Glu Thr Glu Phe Glu Val Arg			
145	150	155	160
gaa ttg gaa gag ttg cct gag gaa tgg cga cgc tcg aag cta gct tgg			528
Glu Leu Glu Glu Leu Pro Glu Glu Trp Arg Arg Ser Lys Leu Ala Trp			
165	170	175	
ctg tgt aaa gag gtt cca acg cat aag gcc gtg acg ctt gtg aga ctc			576
Leu Cys Lys Glu Val Pro Thr His Lys Ala Val Thr Leu Val Arg Leu			
180	185	190	
ttg aat gct cag aag aaa tgg gtt cgt caa gag gac gct act tac atc			624
Leu Asn Ala Gln Lys Lys Trp Val Arg Gln Glu Asp Ala Thr Tyr Ile			
195	200	205	
tct gtt cat tgt atg cga att cgt gag aac gaa act gga ttc agg gtg			672
Ser Val His Cys Met Arg Ile Arg Glu Asn Glu Thr Gly Phe Arg Val			
210	215	220	
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Tyr Arg Trp Met Thr Gln Gln Asn Trp Tyr Arg Phe Asp Phe Gly Leu			
225	230	235	240
acg acg aag cta gct gaa tac ttg ggg aaa gaa cgg aaa ttt acg aaa			768

Thr Thr Lys Leu Ala Glu Tyr Leu Gly Lys Glu Arg Lys Phe Thr Lys
 245 250 255
 tgt cga gag gta ttt gat gat gtt ttg aat caa gga cgt gta cca agt 816
 Cys Arg Glu Val Phe Asp Asp Val Leu Asn Gln Gly Arg Val Pro Ser
 260 265 270
 gaa tct aca ttt cat att ctt gta gtt gcg tat cta agt agc tta tca 864
 Glu Ser Thr Phe His Ile Leu Val Val Ala Tyr Leu Ser Ser Leu Ser
 275 280 285
 gta gaa ggt tgt ctc gag gaa gcg tgt agt gtt tac aat aga atg att 912
 Val Glu Gly Cys Leu Glu Ala Cys Ser Val Tyr Asn Arg Met Ile
 290 295 300
 caa ctt gga ggt tac aaa ccg cgt ctt agt ctg cat aac tct ttg ttt 960
 Gln Leu Gly Gly Tyr Lys Pro Arg Leu Ser Leu His Asn Ser Leu Phe
 305 310 315 320
 aga gct ttg gtt agt aaa caa gga ggg att ctg aat gat cag ctt aag 1008
 Arg Ala Leu Val Ser Lys Gln Gly Ile Leu Asn Asp Gln Leu Lys
 325 330 335
 caa gca gag ttt atc ttt cac aat gtt gtg aca acc ggg ctt gag gtt 1056
 Gln Ala Glu Phe Ile Phe His Asn Val Val Thr Thr Gly Leu Glu Val
 340 345 350
 cag aag gat att tat agt gga ttg atc tgg ctg cat agt tgt caa gat 1104
 Gln Lys Asp Ile Tyr Ser Gly Leu Ile Trp Leu His Ser Cys Gln Asp
 355 360 365
 gaa gtt gat ata ggt agg ata aac tct cta aga gaa gag atg aag aag 1152
 Glu Val Asp Ile Gly Arg Ile Asn Ser Leu Arg Glu Glu Met Lys Lys
 370 375 380
 gcc ggt ttt cag gag agt aaa gaa gtt gtg gta tcg tta ctt aga gct 1200
 Ala Gly Phe Gln Glu Ser Lys Glu Val Val Val Ser Leu Leu Arg Ala
 385 390 395 400
 tat gca aag gag gga ggt gtg gaa gaa gtt gag agg acg tgg ctt gaa 1248
 Tyr Ala Lys Glu Gly Gly Val Glu Glu Val Glu Arg Thr Trp Leu Glu
 405 410 415
 ttg ctt gat tta gat tgt ggt ata cct tct cag gcg ttt gtg tac aaa 1296
 Leu Leu Asp Leu Asp Cys Gly Ile Pro Ser Gln Ala Phe Val Tyr Lys
 420 425 430
 ata gaa gct tat tcg aaa gtc ggc gat ttt gcg aaa gct atg gag ata 1344
 Ile Glu Ala Tyr Ser Lys Val Gly Asp Phe Ala Lys Ala Met Glu Ile
 435 440 445
 ttt agg gag atg gag aag cat ata ggt ggt gca act atg tct gga tac 1392
 Phe Arg Glu Met Glu Lys His Ile Gly Gly Ala Thr Met Ser Gly Tyr
 450 455 460
 cat aaa atc att gag gtt cta tgt aaa gtc caa caa gtg gaa ctt gtg 1440
 His Lys Ile Ile Glu Val Leu Cys Lys Val Gln Gln Val Glu Leu Val
 465 470 475 480
 gaa act ctc atq aaq qaq ttt qaa qaa aqc qqq aaq aaq ccq ctt cta 1488

Glu Thr Leu Met Lys Glu Phe Glu Glu Ser Gly Lys Lys Pro Leu Leu			
485	490	495	
cca tca ttc atc gaa ata gcc aaa atg tac ttc gat ttg ggt tta cat			1536
Pro Ser Phe Ile Glu Ile Ala Lys Met Tyr Phe Asp Leu Gly Leu His			
500	505	510	
gag aaa ttg gag atg gct ttt gtt cag tgc ttg gag aaa tgc caa cct			1584
Glu Lys Leu Glu Met Ala Phe Val Gln Cys Leu Glu Lys Cys Gln Pro			
515	520	525	
agc cag cct ata tat aac ata tat ttg gat tca ttg act aaa ata ggc			1632
Ser Gln Pro Ile Tyr Asn Ile Tyr Leu Asp Ser Leu Thr Lys Ile Gly			
530	535	540	
aac ctt gag aaa gca ggg gat gtc ttc aat gaa atg aaa aac aac ggg			1680
Asn Leu Glu Lys Ala Gly Asp Val Phe Asn Glu Met Lys Asn Asn Gly			
545	550	555	560
aca atc aat gtg agt gct aga tcc tgc aac agc ctt tta aag gga tac			1728
Thr Ile Asn Val Ser Ala Arg Ser Cys Asn Ser Leu Leu Lys Gly Tyr			
565	570	575	
cta gat tgt gga aaa caa gtg cag gca gag aga ata tat gat ctg atg			1776
Leu Asp Cys Gly Lys Gln Val Gln Ala Glu Arg Ile Tyr Asp Leu Met			
580	585	590	
aga atg aag aaa tac gaa atc gaa cca ccg ctt atg gaa aag ctt gat			1824
Arg Met Lys Lys Tyr Glu Ile Glu Pro Pro Leu Met Glu Lys Leu Asp			
595	600	605	
tac atc ctg agc ttg aag aaa gag gtg aag aag aga ccg ttt agc			1872
Tyr Ile Leu Ser Leu Lys Lys Glu Val Lys Lys Arg Pro Phe Ser			
610	615	620	
atg aag cta agc aaa gac cag cgt gag gta ttg gta ggt ttg ttg tta			1920
Met Lys Leu Ser Lys Asp Gln Arg Glu Val Leu Val Gly Leu Leu Leu			
625	630	635	640
ggt ggc ttg caa atc gaa tca gac aaa gag aag aag agc cac atg atc			1968
Gly Gly Leu Gln Ile Glu Ser Asp Lys Glu Lys Lys Ser His Met Ile			
645	650	655	
aaa ttt gaa ttt aga gaa aat tct caa gct cat ctg gtt ctt aaa caa			2016
Lys Phe Glu Phe Arg Glu Asn Ser Gln Ala His Leu Val Leu Lys Gln			
660	665	670	
aac ata cat gac cag ttc cgt gag tgg ttg cat cct ttg agc aat ttt			2064
Asn Ile His Asp Gln Phe Arg Glu Trp Leu His Pro Leu Ser Asn Phe			
675	680	685	
cag gag gat att ata ccg ttc gaa ttc tac tcc gtt ccc cat tca tac			2112
Gln Glu Asp Ile Ile Pro Phe Glu Phe Tyr Ser Val Pro His Ser Tyr			
690	695	700	
ttc ggg ttt tac gct gaa cat tac tgg cca aag ggt cag cca gag att			2160
Phe Gly Phe Tyr Ala Glu His Tyr Trp Pro Lys Gly Gln Pro Glu Ile			
705	710	715	720
cca aaa ctg att cat cgg tgg cta tcg cca cac tca ctc gcg tat tgg			2208

Pro Lys Leu Ile His Arg Trp Leu Ser Pro His Ser Leu Ala Tyr Trp			
725	730	735	
tac atg tac agc ggc gtt aaa aca tca tca gga gac att atc ttg aga			2256
Tyr Met Tyr Ser Gly Val Lys Thr Ser Ser Gly Asp Ile Ile Leu Arg			
740	745	750	
ttg aag gga agt ctc gaa ggt gtt gag aaa gta gta aag gct ctt caa			2304
Leu Lys Gly Ser Leu Glu Gly Val Glu Lys Val Val Lys Ala Leu Gln			
755	760	765	
gcc aaa tct atg gaa tgt cga gtt aag aag aaa gga aaa gtc ttc tgg			2352
Ala Lys Ser Met Glu Cys Arg Val Lys Lys Lys Val Phe Trp			
770	775	780	
att gga ctt cag gga aca aac tca gct ttg ttc tgg aaa cta ata gag			2400
Ile Gly Leu Gln Gly Thr Asn Ser Ala Leu Phe Trp Lys Leu Ile Glu			
785	790	795	800
cct cat gtg tta gag aac ttg aaa gag cat ttg aaa cct gct tct gaa			2448
Pro His Val Leu Glu Asn Leu Lys Glu His Leu Lys Pro Ala Ser Glu			
805	810	815	
tca ctg gac aat gtt aag gaa gca gaa gaa caa agc atc aac ttc aaa			2496
Ser Leu Asp Asn Val Lys Glu Ala Glu Glu Gln Ser Ile Asn Phe Lys			
820	825	830	
tca aac tct gat cac agt gac gat tgt gtc aat tca gaa gca cat ttt			2544
Ser Asn Ser Asp His Ser Asp Asp Cys Val Asn Ser Glu Ala His Phe			
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tac tga			2550
Tyr			

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<212> PRT

<213> *Arabidopsis thaliana*

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Val Ser Val Thr Thr Phe Asn Ile Ser Ser Leu Ser Ser Asn Pro Asn			
35	40	45	

Ile Ile Asn Ser Ser Ser Thr Leu Phe Arg Ser Leu Ser Phe Ser Leu
50 55 60

Ile Arg His Arg Ser Ser Tyr Ser Arg Arg Ser Leu Arg Arg Leu Ser
65 70 75 80

Ile His Thr Val His Gly Asn Lys Thr Gln Phe Phe Ser His Ser Ser
85 90 95

Thr Arg Thr Pro Pro Leu Phe Thr Ala Asn Ser Thr Ala Gln Arg Ser
100 105 110

Gly Thr Phe Val Glu His Leu Thr Gly Ile Thr Glu Ser Glu Glu Gly
115 120 125

Ile Ser Glu Ala Asn Gly Phe Gly Asp Val Glu Ser Ala Arg Asn Asp
130 135 140

Ile Arg Asn Val Ala Thr Arg Arg Ile Glu Thr Glu Phe Glu Val Arg
145 150 155 160

Glu Leu Glu Glu Leu Pro Glu Glu Trp Arg Arg Ser Lys Leu Ala Trp
165 170 175

Leu Cys Lys Glu Val Pro Thr His Lys Ala Val Thr Leu Val Arg Leu
180 185 190

Leu Asn Ala Gln Lys Lys Trp Val Arg Gln Glu Asp Ala Thr Tyr Ile
195 200 205

Ser Val His Cys Met Arg Ile Arg Glu Asn Glu Thr Gly Phe Arg Val
210 215 220

Tyr Arg Trp Met Thr Gln Gln Asn Trp Tyr Arg Phe Asp Phe Gly Leu
225 230 235 240

Thr Thr Lys Leu Ala Glu Tyr Leu Gly Lys Glu Arg Lys Phe Thr Lys
245 250 255

Cys Arg Glu Val Phe Asp Asp Val Leu Asn Gln Gly Arg Val Pro Ser
260 265 270

Glu Ser Thr Phe His Ile Leu Val Val Ala Tyr Leu Ser Ser Leu Ser
275 280 285

Val Glu Gly Cys Leu Glu Glu Ala Cys Ser Val Tyr Asn Arg Met Ile
290 295 300

Gln Leu Gly Gly Tyr Lys Pro Arg Leu Ser Leu His Asn Ser Leu Phe
305 310 315 320

Arg Ala Leu Val Ser Lys Gln Gly Gly Ile Leu Asn Asp Gln Leu Lys
325 330 335

Gln Ala Glu Phe Ile Phe His Asn Val Val Thr Thr Gly Leu Glu Val
340 345 350

Gln Lys Asp Ile Tyr Ser Gly Leu Ile Trp Leu His Ser Cys Gln Asp
355 360 365

Glu Val Asp Ile Gly Arg Ile Asn Ser Leu Arg Glu Glu Met Lys Lys
370 375 380

Ala Gly Phe Gln Glu Ser Lys Glu Val Val Val Ser Leu Leu Arg Ala
385 390 395 400

Tyr Ala Lys Glu Gly Gly Val Glu Glu Val Glu Arg Thr Trp Leu Glu
405 410 415

Leu Leu Asp Leu Asp Cys Gly Ile Pro Ser Gln Ala Phe Val Tyr Lys
420 425 430

Ile Glu Ala Tyr Ser Lys Val Gly Asp Phe Ala Lys Ala Met Glu Ile
435 440 445

Phe Arg Glu Met Glu Lys His Ile Gly Gly Ala Thr Met Ser Gly Tyr
450 455 460

His Lys Ile Ile Glu Val Leu Cys Lys Val Gln Gln Val Glu Leu Val
465 470 475 480

Glu Thr Leu Met Lys Glu Phe Glu Glu Ser Gly Lys Lys Pro Leu Leu
485 490 495

Pro Ser Phe Ile Glu Ile Ala Lys Met Tyr Phe Asp Leu Gly Leu His
500 505 510

Glu Lys Leu Glu Met Ala Phe Val Gln Cys Leu Glu Lys Cys Gln Pro
515 520 525

Ser Gln Pro Ile Tyr Asn Ile Tyr Leu Asp Ser Leu Thr Lys Ile Gly
530 535 540

Asn Leu Glu Lys Ala Gly Asp Val Phe Asn Glu Met Lys Asn Asn Gly
545 550 555 560

Thr Ile Asn Val Ser Ala Arg Ser Cys Asn Ser Leu Leu Lys Gly Tyr
565 570 575

Leu Asp Cys Gly Lys Gln Val Gln Ala Glu Arg Ile Tyr Asp Leu Met
580 585 590

Arg Met Lys Lys Tyr Glu Ile Glu Pro Pro Leu Met Glu Lys Leu Asp
595 600 605

Tyr Ile Leu Ser Leu Lys Lys Glu Val Lys Lys Arg Pro Phe Ser
610 615 620

Met Lys Leu Ser Lys Asp Gln Arg Glu Val Leu Val Gly Leu Leu Leu
625 630 635 640

Gly Gly Leu Gln Ile Glu Ser Asp Lys Glu Lys Lys Ser His Met Ile
645 650 655

Lys Phe Glu Phe Arg Glu Asn Ser Gln Ala His Leu Val Leu Lys Gln
660 665 670

Asn Ile His Asp Gln Phe Arg Glu Trp Leu His Pro Leu Ser Asn Phe
675 680 685

Gln Glu Asp Ile Ile Pro Phe Glu Phe Tyr Ser Val Pro His Ser Tyr
690 695 700

Phe Gly Phe Tyr Ala Glu His Tyr Trp Pro Lys Gly Gln Pro Glu Ile
705 710 715 720

Pro Lys Leu Ile His Arg Trp Leu Ser Pro His Ser Leu Ala Tyr Trp
725 730 735

Tyr Met Tyr Ser Gly Val Lys Thr Ser Ser Gly Asp Ile Ile Leu Arg
740 745 750

Leu Lys Gly Ser Leu Glu Gly Val Glu Lys Val Val Lys Ala Leu Gln
755 760 765

Ala Lys Ser Met Glu Cys Arg Val Lys Lys Lys Gly Lys Val Phe Trp
 770 775 780

Ile Gly Leu Gln Gly Thr Asn Ser Ala Leu Phe Trp Lys Leu Ile Glu
 785 790 795 800

Pro His Val Leu Glu Asn Leu Lys Glu His Leu Lys Pro Ala Ser Glu
 805 810 815

Ser Leu Asp Asn Val Lys Glu Ala Glu Glu Gln Ser Ile Asn Phe Lys
 820 825 830

Ser Asn Ser Asp His Ser Asp Asp Cys Val Asn Ser Glu Ala His Phe
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Tyr

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<213> *Arabidopsis thaliana*

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atc gaa aaa ctc gac atc tta tct gac gac ttc gat cca acc gcc gta 96
 Ile Glu Lys Leu Asp Ile Leu Ser Asp Asp Phe Asp Pro Thr Ala Val
 20 25 30

gtc acc gaa ccg tta cct cct ccg gta act aat gga atc gga gct gat 144
 Val Thr Glu Pro Leu Pro Pro Val Thr Asn Gly Ile Gly Ala Asp
 35 40 45

aaa gga gga gga gga gaa aga gag atg gtt ctc ggt agg aat ata 192
 Lys Gly Gly Gly Gly Glu Arg Glu Met Val Leu Gly Arg Asn Ile
 50 55 60

cac aca acg tca ctc gct gta acg gaa ccg gag gtt aac gat gaa ttc	240
His Thr Thr Ser Leu Ala Val Thr Glu Pro Glu Val Asn Asp Glu Phe	
65 70 75 80	
acc gga gat aaa gaa gct tat atg gct agt gtt ctt gct cgt tac cgg	288
Thr Gly Asp Lys Glu Ala Tyr Met Ala Ser Val Leu Ala Arg Tyr Arg	
85 90 95	
aaa act ttg gtt gaa cga acc aaa aac cat tta ggt tat cct tat aac	336
Lys Thr Leu Val Glu Arg Thr Lys Asn His Leu Gly Tyr Pro Tyr Asn	
100 105 110	
ttg gat ttc gac tat ggt gcg ctt ggt cag tta caa cat ttt tcg att	384
Leu Asp Phe Asp Tyr Gly Ala Leu Gly Gln Leu Gln His Phe Ser Ile	
115 120 125	
aat aat ctt gga gat ccg ttt att gaa agt aac tat ggt gta cac tca	432
Asn Asn Leu Gly Asp Pro Phe Ile Glu Ser Asn Tyr Gly Val His Ser	
130 135 140	
aga cct ttt gaa gtt ggt gtg ttg gat tgg ttt gct cgt ctt tgg gag	480
Arg Pro Phe Glu Val Gly Val Leu Asp Trp Phe Ala Arg Leu Trp Glu	
145 150 155 160	
att gag aga gat gat tat tgg ggt tac att acc aat tgt ggt act gaa	528
Ile Glu Arg Asp Asp Tyr Trp Gly Tyr Ile Thr Asn Cys Gly Thr Glu	
165 170 175	
ggc aac ctt cat ggc att tta gtc ggg agg gag gag atg ttt ccg gat ggg	576
Gly Asn Leu His Gly Ile Leu Val Gly Arg Glu Met Phe Pro Asp Gly	
180 185 190	
ata ttg tat gcg tcg cgt gaa tcg cat tac tcg gtg ttt aaa gct gct	624
Ile Leu Tyr Ala Ser Arg Glu Ser His Tyr Ser Val Phe Lys Ala Ala	
195 200 205	
cga atg tat cga atg gag tgt gag aag gtt gat acg ctt atg tca ggg	672
Arg Met Tyr Arg Met Glu Cys Glu Lys Val Asp Thr Leu Met Ser Gly	
210 215 220	
gag att gat tgt gat ttg agg aag aag ttg ttg gct aat aaa gat	720
Glu Ile Asp Cys Asp Asp Leu Arg Lys Lys Leu Ala Asn Lys Asp	
225 230 235 240	
aaa ccg gcg att ctt aat gtt aac ata gga acg acg gtt aaa gga gct	768
Lys Pro Ala Ile Leu Asn Val Asn Ile Gly Thr Thr Val Lys Gly Ala	
245 250 255	
gtt gat gat ctt gac ctt gtt atc aaa act ctt gaa gag tgt ggt ttc	816
Val Asp Asp Leu Asp Leu Val Ile Lys Thr Leu Glu Glu Cys Gly Phe	
260 265 270	
tca cat gat agg ttc tat att cat tgt gat gga gct ttg ttt gga ctt	864
Ser His Asp Arg Phe Tyr Ile His Cys Asp Gly Ala Leu Phe Gly Leu	
275 280 285	
atg atg cct ttt gtc aaa cgt gca ccg aaa gtg acg ttt aat aaa ccg	912
Met Met Pro Phe Val Lys Arg Ala Pro Lys Val Thr Phe Asn Lys Pro	
290 295 300	

ata ggg agt gtg agt gta tcg ggc cac aaa ttt gtc ggg tgt cca atg Ile Gly Ser Val Ser Val Ser Gly His Lys Phe Val Gly Cys Pro Met 305 310 315 320	960
cca tgt ggt gtt cag ata aca aga atg gaa cat atc aaa gtc ctc tcc Pro Cys Gly Val Gln Ile Thr Arg Met Glu His Ile Lys Val Leu Ser 325 330 335	1008
agt aac gtt gag tac ctt gct tca agg gat gca aca atc atg gga agt Ser Asn Val Glu Tyr Leu Ala Ser Arg Asp Ala Thr Ile Met Gly Ser 340 345 350	1056
cgt aac ggg cat gct cct ttg ttc ctc tgg tac acc tta aac agg aaa Arg Asn Gly His Ala Pro Leu Phe Leu Trp Tyr Thr Leu Asn Arg Lys 355 360 365	1104
ggg tac aaa gga ttc cag aaa gaa gtt cag aaa tgc ttg aga aac gcg Gly Tyr Lys Gly Phe Gln Lys Glu Val Gln Lys Cys Leu Arg Asn Ala 370 375 380	1152
cat tac ctc aaa gac cga ctt cgt gaa gct ggg att agc gcc atg ctt His Tyr Leu Lys Asp Arg Leu Arg Glu Ala Gly Ile Ser Ala Met Leu 385 390 395 400	1200
aat gag ctt agc agc act gtg gtc ttt gaa cgg cct aaa gat gaa gag Asn Glu Leu Ser Ser Thr Val Val Phe Glu Arg Pro Lys Asp Glu Glu 405 410 415	1248
ttt gtt aga agg tgg cag ctt gct tgc caa ggt gat ata gct cat gtg Phe Val Arg Arg Trp Gln Leu Ala Cys Gln Gly Asp Ile Ala His Val 420 425 430	1296
gtg gtt atg cca agt gtt aca atc gag aag ctt gat aat ttc ctg aaa Val Val Met Pro Ser Val Thr Ile Glu Lys Leu Asp Asn Phe Leu Lys 435 440 445	1344
gac ctt gtc aaa cac aga ttg atc tgg tac gag gat gga tct cag cct Asp Leu Val Lys His Arg Leu Ile Trp Tyr Glu Asp Gly Ser Gln Pro 450 455 460	1392
cct tgc ctt gca tcg gag gta gga acc aac aac tgc atc tgt cca gct Pro Cys Leu Ala Ser Glu Val Gly Thr Asn Asn Cys Ile Cys Pro Ala 465 470 475 480	1440
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Val Thr Glu Pro Leu Pro Pro Val Thr Asn Gly Ile Gly Ala Asp
35 40 45

Lys Gly Gly Gly Gly Glu Arg Glu Met Val Leu Gly Arg Asn Ile
50 55 60

His Thr Thr Ser Leu Ala Val Thr Glu Pro Glu Val Asn Asp Glu Phe
65 70 75 80

Thr Gly Asp Lys Glu Ala Tyr Met Ala Ser Val Leu Ala Arg Tyr Arg
85 90 95

Lys Thr Leu Val Glu Arg Thr Lys Asn His Leu Gly Tyr Pro Tyr Asn
100 105 110

Leu Asp Phe Asp Tyr Gly Ala Leu Gly Gln Leu Gln His Phe Ser Ile
115 120 125

Asn Asn Leu Gly Asp Pro Phe Ile Glu Ser Asn Tyr Gly Val His Ser
130 135 140

Arg Pro Phe Glu Val Gly Val Leu Asp Trp Phe Ala Arg Leu Trp Glu
145 150 155 160

Ile Glu Arg Asp Asp Tyr Trp Gly Tyr Ile Thr Asn Cys Gly Thr Glu
165 170 175

Gly Asn Leu His Gly Ile Leu Val Gly Arg Glu Met Phe Pro Asp Gly
180 185 190

Ile Leu Tyr Ala Ser Arg Glu Ser His Tyr Ser Val Phe Lys Ala Ala
195 200 205

Arg Met Tyr Arg Met Glu Cys Glu Lys Val Asp Thr Leu Met Ser Gly
210 215 220

Glu Ile Asp Cys Asp Asp Leu Arg Lys Lys Leu Leu Ala Asn Lys Asp
225 230 235 240

Lys Pro Ala Ile Leu Asn Val Asn Ile Gly Thr Thr Val Lys Gly Ala
245 250 255

Val Asp Asp Leu Asp Leu Val Ile Lys Thr Leu Glu Glu Cys Gly Phe
260 265 270

Ser His Asp Arg Phe Tyr Ile His Cys Asp Gly Ala Leu Phe Gly Leu
275 280 285

Met Met Pro Phe Val Lys Arg Ala Pro Lys Val Thr Phe Asn Lys Pro
290 295 300

Ile Gly Ser Val Ser Val Ser Gly His Lys Phe Val Gly Cys Pro Met
305 310 315 320

Pro Cys Gly Val Gln Ile Thr Arg Met Glu His Ile Lys Val Leu Ser
325 330 335

Ser Asn Val Glu Tyr Leu Ala Ser Arg Asp Ala Thr Ile Met Gly Ser
340 345 350

Arg Asn Gly His Ala Pro Leu Phe Leu Trp Tyr Thr Leu Asn Arg Lys
355 360 365

Gly Tyr Lys Gly Phe Gln Lys Glu Val Gln Lys Cys Leu Arg Asn Ala
370 375 380

His Tyr Leu Lys Asp Arg Leu Arg Glu Ala Gly Ile Ser Ala Met Leu
385 390 395 400

Asn Glu Leu Ser Ser Thr Val Val Phe Glu Arg Pro Lys Asp Glu Glu
405 410 415

Phe Val Arg Arg Trp Gln Leu Ala Cys Gln Gly Asp Ile Ala His Val
420 425 430

Val Val Met Pro Ser Val Thr Ile Glu Lys Leu Asp Asn Phe Leu Lys
435 440 445

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His Lys

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ctt agc tcg aag aaa tct gga aag gga aag aga cct gga aaa ggt gga		96
Leu Ser Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly Gly		
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aac cgt ttc tgg aag aac att ggt ttg ggc ttc aag act cct cgt gaa		144
Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu		
35 40 45		
gcc att gat gga gct tac gtt gac aag aaa tgc ccc ttc act gga act		192
Ala Ile Asp Gly Ala Tyr Val Asp Lys Lys Cys Pro Phe Thr Gly Thr		
50 55 60		
gtt tcc att aga ggt cgt atc tta gct ggt act tgc cac agt gcg aaa		240
Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys His Ser Ala Lys		
65 70 75 80		
atg cag agg acc att atc gtg cga agg gat tac ctt cac ttt gtg aag		288
Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu His Phe Val Lys		
85 90 95		
aag tat cag agg tat gag aag agg cat tca aac att ccg gct cat gtc		336
Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His Val		
100 105 110		
tca cca tgc ttc cgt gtt aag gaa gga gac cat atc atc att ggc caa		384
Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Ile Ile Gly Gln		
115 120 125		
tgc agg cca ttg tcg aag aca gtg agg ttc aat gtg ttg aag gtg ata		432

Cys	Arg	Pro	Leu	Ser	Lys	Thr	Val	Arg	Phe	Asn	Val	Leu	Lys	Val	Ile	
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cca	gct	ggg	tct	tct	tca	ttt	gga	aag	aag	gca	ttc	act	gga	atg		480
Pro	Ala	Gly	Ser	Ser	Ser	Ser	Phe	Gly	Lys	Lys	Ala	Phe	Thr	Gly	Met	
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taa																483
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			20				25						30			
Asn	Arg	Phe	Trp	Lys	Asn	Ile	Gly	Leu	Gly	Phe	Lys	Thr	Pro	Arg	Glu	
			35				40						45			
Ala	Ile	Asp	Gly	Ala	Tyr	Val	Asp	Lys	Lys	Cys	Pro	Phe	Thr	Gly	Thr	
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Val	Ser	Ile	Arg	Gly	Arg	Ile	Leu	Ala	Gly	Thr	Cys	His	Ser	Ala	Lys	
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Met	Gln	Arg	Thr	Ile	Ile	Val	Arg	Arg	Asp	Tyr	Leu	His	Phe	Val	Lys	
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Lys	Tyr	Gln	Arg	Tyr	Glu	Lys	Arg	His	Ser	Asn	Ile	Pro	Ala	His	Val	
						100							105		110	
Ser	Pro	Cys	Phe	Arg	Val	Lys	Glu	Gly	Asp	His	Ile	Ile	Ile	Gly	Gln	
						115							120		125	
Cys	Arg	Pro	Leu	Ser	Lys	Thr	Val	Arg	Phe	Asn	Val	Leu	Lys	Val	Ile	
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Pro	Ala	Gly	Ser	Ser	Ser	Ser	Phe	Gly	Lys	Lys	Ala	Phe	Thr	Gly	Met	
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 <223> 10708

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Met Ser His Arg Lys Phe Glu His Pro Arg His Gly Ser Leu Gly Phe		
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ctt cca agg aag aga gct aac cgt cac aga gga aag gtg aag gcg ttc		96
Leu Pro Arg Lys Arg Ala Asn Arg His Arg Gly Lys Val Lys Ala Phe		
20 25 30		
cct aag gat gac caa acc aag cct tgc aag ttc aca gct ttc atg ggt		144
Pro Lys Asp Asp Gln Thr Lys Pro Cys Lys Phe Thr Ala Phe Met Gly		
35 40 45		
tac aaa gct ggt atg act cac att gtc aga gaa gtg gag aaa cct gga		192
Tyr Lys Ala Gly Met Thr His Ile Val Arg Glu Val Glu Lys Pro Gly		
50 55 60		
tcc aag ctt cac aag aag gag aca tgt gag gct gtt acc atc att gag		240
Ser Lys Leu His Lys Glu Thr Cys Glu Ala Val Thr Ile Ile Glu		
65 70 75 80		
aca cct gct atg gtg gtt gga gtt gtt gcc tat gtg aag act cct		288
Thr Pro Ala Met Val Val Gly Val Val Ala Tyr Val Lys Thr Pro		
85 90 95		
aga ggt ttg agg tct ttg aac act gtc tgg gca cag cat ttg agt gag		336
Arg Gly Leu Arg Ser Leu Asn Thr Val Trp Ala Gln His Leu Ser Glu		
100 105 110		
gag gtc agg aga agg ttc tac aag aac tgg gct aag tct aag aag aag		384
Glu Val Arg Arg Phe Tyr Lys Asn Trp Ala Lys Ser Lys Lys Lys		
115 120 125		
gct ttc act ggg tac gct aag cag tat gac agt gag gat ggc aag aag		432
Ala Phe Thr Gly Tyr Ala Lys Gln Tyr Asp Ser Glu Asp Gly Lys Lys		
130 135 140		
ggt att cag gct cag ctt gag aag atg aag tac gtc act gtc atc		480

Gly Ile Gln Ala Gln Leu Glu Lys Met Lys Lys Tyr Ala Thr Val Ile			
145	150	155	160
cgt gtt ttg gct cac act cag atc agg aag atg aag gga ttg aag cag			528
Arg Val Leu Ala His Thr Gln Ile Arg Lys Met Lys Gly Leu Lys Gln			
165	170	175	
aag aag gct cac atg atg gag atc cag atc aat ggt ggt acc att gcc			576
Lys Lys Ala His Met Met Glu Ile Gln Ile Asn Gly Gly Thr Ile Ala			
180	185	190	
cag aag gtt gac ttt gcc tac agt ttc ttt gag aag cag atc cca att			624
Gln Lys Val Asp Phe Ala Tyr Ser Phe Phe Glu Lys Gln Ile Pro Ile			
195	200	205	
gaa gct gtc ttc cag aag gat gaa atg att gat atc att ggt gtg acc			672
Glu Ala Val Phe Gln Lys Asp Glu Met Ile Asp Ile Ile Gly Val Thr			
210	215	220	
aag ggt aag ggt tat gaa ggt gtt act cgt tgg ggt gtt acc cgt			720
Lys Gly Lys Gly Tyr Glu Gly Val Val Thr Arg Trp Gly Val Thr Arg			
225	230	235	240
ctt cct cgt aag act cac aga ggt ctg cgt aag gtt gct tgt att ggt			768
Leu Pro Arg Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly			
245	250	255	
gcg tgg cat cct gct aga gtg tcc tac act gtt gct agg gct ggt cag			816
Ala Trp His Pro Ala Arg Val Ser Tyr Thr Val Ala Arg Ala Gly Gln			
260	265	270	
aac ggt tac cat cac cgt act gag ctt aac aag aag att tac agg ttg			864
Asn Gly Tyr His His Arg Thr Glu Leu Asn Lys Lys Ile Tyr Arg Leu			
275	280	285	
ggt aag gtt ggt act gag gca cac aca gcc atg act gaa tat gac agg			912
Gly Lys Val Gly Thr Glu Ala His Thr Ala Met Thr Glu Tyr Asp Arg			
290	295	300	
act gag aag gat gtg act cca atg gga ggc ttc cca cac tac ggt att			960
Thr Glu Lys Asp Val Thr Pro Met Gly Gly Phe Pro His Tyr Gly Ile			
305	310	315	320
gtg aag gat gac tac ttg atg att aag ggg tgc tgt gtt ggt ccc aag			1008
Val Lys Asp Asp Tyr Leu Met Ile Lys Gly Cys Cys Val Gly Pro Lys			
325	330	335	
aag aga gtt gta act ctc aga cag tca ctt ctc act cag act tcc cgt			1056
Lys Arg Val Val Thr Leu Arg Gln Ser Leu Leu Thr Gln Thr Ser Arg			
340	345	350	
ctt gcc ttg gag gag atc aaa ctc aag ttt att gac acc gcc tcc att			1104
Leu Ala Leu Glu Glu Ile Lys Leu Lys Phe Ile Asp Thr Ala Ser Ile			
355	360	365	
ttt gga cat ggt cgc ttc cag acc tcc ctt gag aag atg agg ttt tac			1152
Phe Gly His Gly Arg Phe Gln Thr Ser Leu Glu Lys Met Arg Phe Tyr			
370	375	380	
aac cgt gtc acg aag taa			1170

Asn Arg Val Thr Lys
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<210> 14

<211> 389

<212> PRT

<213> *Arabidopsis thaliana*

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Pro Lys Asp Asp Gln Thr Lys Pro Cys Lys Phe Thr Ala Phe Met Gly
35 40 45

Tyr Lys Ala Gly Met Thr His Ile Val Arg Glu Val Glu Lys Pro Gly
50 55 60

Ser Lys Leu His Lys Lys Glu Thr Cys Glu Ala Val Thr Ile Ile Glu
65 70 75 80

Thr Pro Ala Met Val Val Val Gly Val Val Ala Tyr Val Lys Thr Pro
85 90 95

Arg Gly Leu Arg Ser Leu Asn Thr Val Trp Ala Gln His Leu Ser Glu
100 105 110

Glu Val Arg Arg Arg Phe Tyr Lys Asn Trp Ala Lys Ser Lys Lys Lys
115 120 125

Ala Phe Thr Gly Tyr Ala Lys Gln Tyr Asp Ser Glu Asp Gly Lys Lys
130 135 140

Gly Ile Gln Ala Gln Leu Glu Lys Met Lys Lys Tyr Ala Thr Val Ile
145 150 155 160

Arg Val Leu Ala His Thr Gln Ile Arg Lys Met Lys Gly Leu Lys Gln
165 170 175

Lys Lys Ala His Met Met Glu Ile Gln Ile Asn Gly Gly Thr Ile Ala
180 185 190

Gln Lys Val Asp Phe Ala Tyr Ser Phe Phe Glu Lys Gln Ile Pro Ile
195 200 205

Glu Ala Val Phe Gln Lys Asp Glu Met Ile Asp Ile Ile Gly Val Thr
210 215 220

Lys Gly Lys Gly Tyr Glu Gly Val Val Thr Arg Trp Gly Val Thr Arg
225 230 235 240

Leu Pro Arg Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly
245 250 255

Ala Trp His Pro Ala Arg Val Ser Tyr Thr Val Ala Arg Ala Gly Gln
260 265 270

Asn Gly Tyr His His Arg Thr Glu Leu Asn Lys Lys Ile Tyr Arg Leu
275 280 285

Gly Lys Val Gly Thr Glu Ala His Thr Ala Met Thr Glu Tyr Asp Arg
290 295 300

Thr Glu Lys Asp Val Thr Pro Met Gly Gly Phe Pro His Tyr Gly Ile
305 310 315 320

Val Lys Asp Asp Tyr Leu Met Ile Lys Gly Cys Cys Val Gly Pro Lys
325 330 335

Lys Arg Val Val Thr Leu Arg Gln Ser Leu Leu Thr Gln Thr Ser Arg
340 345 350

Leu Ala Leu Glu Glu Ile Lys Leu Lys Phe Ile Asp Thr Ala Ser Ile
355 360 365

Phe Gly His Gly Arg Phe Gln Thr Ser Leu Glu Lys Met Arg Phe Tyr
370 375 380

Asn Arg Val Thr Lys
385

<210> 15

<211> 351

<212> DNA

<213> Arabidopsis thaliana

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<221> CDS

<222> (1)..(351)

<223> 10844

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Met Lys Pro Val Ile Gly Thr Val Val Ser Asn Lys Met Gln Lys Ser	
1 5 10 15	

gta gtg gtc gcc gtc gat aga ctc ttc cac aac aaa atc tac aat cgc	96
Val Val Val Ala Val Asp Arg Leu Phe His Asn Lys Ile Tyr Asn Arg	
20 25 30	

tac gtc aaa cga act tcc aaa ttc atg gct cac gac gac aaa gac gcc	144
Tyr Val Lys Arg Thr Ser Lys Phe Met Ala His Asp Asp Lys Asp Ala	
35 40 45	

tgc aac atc ggc gat cga gtg aag tta gat cca tca agg cct ttg agc	192
Cys Asn Ile Gly Asp Arg Val Lys Leu Asp Pro Ser Arg Pro Leu Ser	
50 55 60	

aag aat aag cat tgg att gtt gca gaa atc atc aaa aaa gct cga att	240
Lys Asn Lys His Trp Ile Val Ala Glu Ile Ile Lys Lys Ala Arg Ile	
65 70 75 80	

tat tct cct aaa gct gct gct gct gtt tct gct tct gct tct gct	288
Tyr Ser Pro Lys Ala Ala Ala Ala Val Ser Ala Ser Ala Ser Ala	
85 90 95	

tcc tca gcc tcc act act gac tct tct gct cag tct cag att cct cca	336
Ser Ser Ala Ser Thr Thr Asp Ser Ser Ala Gln Ser Gln Ile Pro Pro	
100 105 110	

tca tct act tct taa	351
Ser Ser Thr Ser	
115	

<210> 16

<211> 116

<212> PRT

<213> Arabidopsis thaliana

<400> 16

Met	Lys	Pro	Val	Ile	Gly	Thr	Val	Val	Ser	Asn	Lys	Met	Gln	Lys	Ser
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Val	Val	Val	Ala	Val	Asp	Arg	Leu	Phe	His	Asn	Lys	Ile	Tyr	Asn	Arg
							20			25			30		

Tyr	Val	Lys	Arg	Thr	Ser	Lys	Phe	Met	Ala	His	Asp	Asp	Lys	Asp	Ala
						35		40				45			

Cys	Asn	Ile	Gly	Asp	Arg	Val	Lys	Leu	Asp	Pro	Ser	Arg	Pro	Leu	Ser
						50		55		60					

Lys	Asn	Lys	His	Trp	Ile	Val	Ala	Glu	Ile	Ile	Lys	Lys	Ala	Arg	Ile
					65		70		75				80		

Tyr	Ser	Pro	Lys	Ala	Ala	Ala	Ala	Val	Ser	Ala	Ser	Ala	Ser	Ala	
					85		90		95						

Ser	Ser	Ala	Ser	Thr	Thr	Asp	Ser	Ser	Ala	Gln	Ser	Gln	Ile	Pro	Pro
					100			105				110			

Ser	Ser	Thr	Ser												
			115												

<210> 17

<211> 1269

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (1)..(1269)

<223> 10951

<400> 17

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Met	Ser	Ser	Ser	Val	Ala	Val	Leu	Trp	Val	Ala	Thr	Ser	Ser	Leu	Asn
1				5					10				15		

48

cca	gac	cca	atg	aac	aat	tgt	ggg	ttg	gta	agg	gtt	cta	gaa	tct	tct
Pro	Asp	Pro	Met	Asn	Asn	Cys	Gly	Leu	Val	Arg	Val	Leu	Glu	Ser	Ser

96

20	25	30	
aga ctg ttc tct cct tgt cag aat cag aga cta aac aaa ggt aag aag			144
Arg Leu Phe Ser Pro Cys Gln Asn Gln Arg Leu Asn Lys Gly Lys Lys			
35	40	45	
aag cag ata cca act tgg agt tct tct ttt gta agg aac cga agt aga			192
Lys Gln Ile Pro Thr Trp Ser Ser Ser Phe Val Arg Asn Arg Ser Arg			
50	55	60	
aga att ggt gtt gtg tct tca agc tta gta gca agt cct tct gga gag			240
Arg Ile Gly Val Val Ser Ser Ser Leu Val Ala Ser Pro Ser Gly Glu			
65	70	75	80
ata gct ctt tca tct gaa gag aag gtt tac aat gtt gtg ttg aaa caa			288
Ile Ala Leu Ser Ser Glu Glu Lys Val Tyr Asn Val Val Leu Lys Gln			
85	90	95	
gct gct ttg gtg aac aaa cag cta agg tct tct tat gac ctt gat			336
Ala Ala Leu Val Asn Lys Gln Leu Arg Ser Ser Ser Tyr Asp Leu Asp			
100	105	110	
gtg aag aaa cca caa gat gtt gtt ctt cct ggg agt ttg agt ttg ttg			384
Val Lys Lys Pro Gln Asp Val Val Leu Pro Gly Ser Leu Ser Leu Leu			
115	120	125	
ggt gaa gct tat gat cga tgc ggt gaa gtt tgc gct gaa tat cct aag			432
Gly Glu Ala Tyr Asp Arg Cys Gly Glu Val Cys Ala Glu Tyr Pro Lys			
130	135	140	
acg ttt tat ctt gga act ttg ctt atg aca ccc gaa agg cga aag gcg			480
Thr Phe Tyr Leu Gly Thr Leu Leu Met Thr Pro Glu Arg Arg Lys Ala			
145	150	155	160
att tgg gca atc tac gtt tgg tgt aga aga act gat gaa ctt gtg gat			528
Ile Trp Ala Ile Tyr Val Trp Cys Arg Arg Thr Asp Glu Leu Val Asp			
165	170	175	
ggg cca aat gct tca cat ata act ccc atg gct tta gat aga tgg gaa			576
Gly Pro Asn Ala Ser His Ile Thr Pro Met Ala Leu Asp Arg Trp Glu			
180	185	190	
gca agg tta gaa gat ctt ttc cgt ggt cgt cct ttc gat atg ctt gat			624
Ala Arg Leu Glu Asp Leu Phe Arg Gly Arg Pro Phe Asp Met Leu Asp			
195	200	205	
gct gct ctc gct gat aca gtt gct aga tac ccg gtc gat att cag cca			672
Ala Ala Leu Ala Asp Thr Val Ala Arg Tyr Pro Val Asp Ile Gln Pro			
210	215	220	
ttt cga gac atc gaa gga atg aga atg gac ttg aag aaa tcg aga			720
Phe Arg Asp Met Ile Glu Gly Met Arg Met Asp Leu Lys Lys Ser Arg			
225	230	235	240
tac cag aac ttc gat gat cta tac ctt tac tgc tac tac gtc gct gga			768
Tyr Gln Asn Phe Asp Asp Leu Tyr Leu Tyr Cys Tyr Tyr Val Ala Gly			
245	250	255	
acc gtc gga ttg atg agc gtt ccg gtt atg gga atc gat cct aag tcg			816
Thr Val Gly Leu Met Ser Val Pro Val Met Gly Ile Asp Pro Lys Ser			

260	265	270	
aaa gca aca acc gaa agt gtt tac aac gct gcc ttg gcc ctt ggt ata Lys Ala Thr Thr Glu Ser Val Tyr Asn Ala Ala Leu Ala Leu Gly Ile 275	280	285	864
gcc aat cag ctt act aac ata ctc aga gac gta ggc gaa gat gcg aga Ala Asn Gln Leu Thr Asn Ile Leu Arg Asp Val Gly Glu Asp Ala Arg 290	295	300	912
aga gga agg gtt tat ctg cct cag gat gaa ttg gct cag gct ggt ctt Arg Gly Arg Val Tyr Leu Pro Gln Asp Glu Leu Ala Gln Ala Gly Leu 305	310	315	960
tca gat gaa gac ata ttc gcc gga aaa gta act gat aaa tgg aga aac Ser Asp Glu Asp Ile Phe Ala Gly Lys Val Thr Asp Lys Trp Arg Asn 325	330	335	1008
ttc atg aaa atg cag ctt aaa cga gca aga atg ttc ttc gac gaa gct Phe Met Lys Met Gln Leu Lys Arg Ala Arg Met Phe Phe Asp Glu Ala 340	345	350	1056
gag aaa ggc gtc acc gag ctc agt gcc gct agc aga tgg cct gta tgg Glu Lys Gly Val Thr Glu Leu Ser Ala Ala Ser Arg Trp Pro Val Trp 355	360	365	1104
gct tca ttg cta ttg tac agg aga ata ctg gac gag att gaa gcg aat Ala Ser Leu Leu Tyr Arg Arg Ile Leu Asp Glu Ile Glu Ala Asn 370	375	380	1152
gat tac aac aat ttt act aag aga gct tat gtg ggg aaa gtc aag aaa Asp Tyr Asn Asn Phe Thr Lys Arg Ala Tyr Val Gly Lys Val Lys Lys 385	390	395	1200
att gca gct ttg cca ttg gct tat gct aaa tca gta cta aag act tca Ile Ala Ala Leu Pro Leu Ala Tyr Ala Lys Ser Val Leu Lys Thr Ser 405	410	415	1248
agt tca aga cta tcg ata tga Ser Ser Arg Leu Ser Ile 420			1269
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Pro Asp Pro Met Asn Asn Cys Gly Leu Val Arg Val Leu Glu Ser Ser			

20

25

30

Arg Leu Phe Ser Pro Cys Gln Asn Gln Arg Leu Asn Lys Gly Lys Lys
35 40 45

Lys Gln Ile Pro Thr Trp Ser Ser Ser Phe Val Arg Asn Arg Ser Arg
50 55 60

Arg Ile Gly Val Val Ser Ser Ser Leu Val Ala Ser Pro Ser Gly Glu
65 70 75 80

Ile Ala Leu Ser Ser Glu Glu Lys Val Tyr Asn Val Val Leu Lys Gln
85 90 95

Ala Ala Leu Val Asn Lys Gln Leu Arg Ser Ser Tyr Asp Leu Asp
100 105 110

Val Lys Lys Pro Gln Asp Val Val Leu Pro Gly Ser Leu Ser Leu Leu
115 120 125

Gly Glu Ala Tyr Asp Arg Cys Gly Glu Val Cys Ala Glu Tyr Pro Lys
130 135 140

Thr Phe Tyr Leu Gly Thr Leu Leu Met Thr Pro Glu Arg Arg Lys Ala
145 150 155 160

Ile Trp Ala Ile Tyr Val Trp Cys Arg Arg Thr Asp Glu Leu Val Asp
165 170 175

Gly Pro Asn Ala Ser His Ile Thr Pro Met Ala Leu Asp Arg Trp Glu
180 185 190

Ala Arg Leu Glu Asp Leu Phe Arg Gly Arg Pro Phe Asp Met Leu Asp
195 200 205

Ala Ala Leu Ala Asp Thr Val Ala Arg Tyr Pro Val Asp Ile Gln Pro
210 215 220

Phe Arg Asp Met Ile Glu Gly Met Arg Met Asp Leu Lys Lys Ser Arg
225 230 235 240

Tyr Gln Asn Phe Asp Asp Leu Tyr Leu Tyr Cys Tyr Tyr Val Ala Gly
245 250 255

Thr Val Gly Leu Met Ser Val Pro Val Met Gly Ile Asp Pro Lys Ser

260

265

270

Lys Ala Thr Thr Glu Ser Val Tyr Asn Ala Ala Leu Ala Leu Gly Ile
275 280 285

Ala Asn Gln Leu Thr Asn Ile Leu Arg Asp Val Gly Glu Asp Ala Arg
290 295 300

Arg Gly Arg Val Tyr Leu Pro Gln Asp Glu Leu Ala Gln Ala Gly Leu
305 310 315 320

Ser Asp Glu Asp Ile Phe Ala Gly Lys Val Thr Asp Lys Trp Arg Asn
325 330 335

Phe Met Lys Met Gln Leu Lys Arg Ala Arg Met Phe Phe Asp Glu Ala
340 345 350

Glu Lys Gly Val Thr Glu Leu Ser Ala Ala Ser Arg Trp Pro Val Trp
355 360 365

Ala Ser Leu Leu Leu Tyr Arg Arg Ile Leu Asp Glu Ile Glu Ala Asn
370 375 380

Asp Tyr Asn Asn Phe Thr Lys Arg Ala Tyr Val Gly Lys Val Lys Lys
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Ile Ala Ala Leu Pro Leu Ala Tyr Ala Lys Ser Val Leu Lys Thr Ser
405 410 415

Ser Ser Arg Leu Ser Ile
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<212> DNA

<213> *Arabidopsis thaliana*

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gct aac gac gcc gaa caa atc cct tat tct tcg ttc gtc gtc gac acg	96		
Ala Asn Asp Ala Glu Gln Ile Pro Tyr Ser Ser Phe Val Val Asp Thr			
20 25 30			
tct ttg cct ctt cct ctc atg att cct cgt atc ata gag tta tgt aaa	144		
Ser Leu Pro Leu Pro Leu Met Ile Pro Arg Ile Ile Glu Leu Cys Lys			
35 40 45			
gat ctg ttc aag aat tgg gga gag ctt gat gat tca ctc ttc tct gtt	192		
Asp Leu Phe Lys Asn Trp Gly Glu Leu Asp Asp Ser Leu Phe Ser Val			
50 55 60			
gag aga gta tct gga ggc att aca aat ctt ttg ctg aag gtt tct gtg	240		
Glu Arg Val Ser Gly Gly Ile Thr Asn Leu Leu Leu Lys Val Ser Val			
65 70 75 80			
aaa gag gac act aat aaa gaa gtg tct gtt aca gtg aga ctg tat ggg	288		
Lys Glu Asp Thr Asn Lys Glu Val Ser Val Thr Val Arg Leu Tyr Gly			
85 90 95			
cct aac act gag tat gtt att aac cgg gag aga gag att ctg gct atc	336		
Pro Asn Thr Glu Tyr Val Ile Asn Arg Glu Arg Glu Ile Leu Ala Ile			
100 105 110			
aag tat ctc tcg gct gcc gga ttt ggt gcc aag ttg ctt ggt ggt ttt	384		
Lys Tyr Leu Ser Ala Ala Gly Phe Gly Ala Lys Leu Leu Gly Gly Phe			
115 120 125			
gga aat ggc atg gtg caa tcg ttc atc aat gca aga acc tta gag cca	432		
Gly Asn Gly Met Val Gln Ser Phe Ile Asn Ala Arg Thr Leu Glu Pro			
130 135 140			
tca gac atg aga gag cca aag att gct gca caa att gcc aga gaa ctt	480		
Ser Asp Met Arg Glu Pro Lys Ile Ala Ala Gln Ile Ala Arg Glu Leu			
145 150 155 160			
gga aag ttt cat aaa gtg gac ata cca ggt tcc aag gaa cct cag ctg	528		
Gly Lys Phe His Lys Val Asp Ile Pro Gly Ser Lys Glu Pro Gln Leu			
165 170 175			
tgg gtt gat atc ttg aag ttc tat gaa aaa gca tct act ctt acg ttt	576		
Trp Val Asp Ile Leu Lys Phe Tyr Glu Lys Ala Ser Thr Leu Thr Phe			
180 185 190			
gaa gaa cct gat aag cag aag ctc ttt gag act att tcg ttt gaa gaa	624		
Glu Glu Pro Asp Lys Gln Lys Leu Phe Glu Thr Ile Ser Phe Glu Glu			
195 200 205			
ctc cac aaa gaa att att gag cta agg gaa ttc aca ggc tta ctt aac	672		
Leu His Lys Glu Ile Ile Glu Leu Arg Glu Phe Thr Gly Leu Leu Asn			
210 215 220			

gca cct gtg gtg ttt gct cat aac gat tta cta tca gga aac ttc atg Ala Pro Val Val Phe Ala His Asn Asp Leu Leu Ser Gly Asn Phe Met 225 230 235 240	720
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tca tac aac tat aga ggc ttt gac atc gga aat cac ttc aat gaa tat Ser Tyr Asn Tyr Arg Gly Phe Asp Ile Gly Asn His Phe Asn Glu Tyr 260 265 270	816
gca gga tac gac tgt gat tac agc ctg tac cca agt aaa gag gaa caa Ala Gly Tyr Asp Cys Asp Tyr Ser Leu Tyr Pro Ser Lys Glu Glu Gln 275 280 285	864
tat cat ttc atc aag cat tac tta cag cca gac aaa cca gac gag gtc Tyr His Phe Ile Lys His Tyr Leu Gln Pro Asp Lys Pro Asp Glu Val 290 295 300	912
agt atc gct gaa gta gaa tca gtc ttt gta gag aca gat gcg tat aaa Ser Ile Ala Glu Val Glu Ser Val Phe Val Glu Thr Asp Ala Tyr Lys 305 310 315 320	960
tta gca tct cat ttg tac tgg gca ata tgg gcg atc atc cag gca agg Leu Ala Ser His Leu Tyr Trp Ala Ile Trp Ala Ile Ile Gln Ala Arg 325 330 335	1008
atg tct ccc att gag ttt gaa tat ttg ggt tac ttc ttt ttg cgg tac Met Ser Pro Ile Glu Phe Glu Tyr Leu Gly Tyr Phe Phe Leu Arg Tyr 340 345 350	1056
aat gaa tac aag aag cag aag cca ctt act ttt tca ctt gtt aca tct Asn Glu Tyr Lys Lys Gln Lys Pro Leu Thr Phe Ser Leu Val Thr Ser 355 360 365	1104
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35 40 45

Asp Leu Phe Lys Asn Trp Gly Glu Leu Asp Asp Ser Leu Phe Ser Val
50 55 60

Glu Arg Val Ser Gly Gly Ile Thr Asn Leu Leu Leu Lys Val Ser Val
65 70 75 80

Lys Glu Asp Thr Asn Lys Glu Val Ser Val Thr Val Arg Leu Tyr Gly
85 90 95

Pro Asn Thr Glu Tyr Val Ile Asn Arg Glu Arg Glu Ile Leu Ala Ile
100 105 110

Lys Tyr Leu Ser Ala Ala Gly Phe Gly Ala Lys Leu Leu Gly Gly Phe
115 120 125

Gly Asn Gly Met Val Gln Ser Phe Ile Asn Ala Arg Thr Leu Glu Pro
130 135 140

Ser Asp Met Arg Glu Pro Lys Ile Ala Ala Gln Ile Ala Arg Glu Leu
145 150 155 160

Gly Lys Phe His Lys Val Asp Ile Pro Gly Ser Lys Glu Pro Gln Leu
165 170 175

Trp Val Asp Ile Leu Lys Phe Tyr Glu Lys Ala Ser Thr Leu Thr Phe
180 185 190

Glu Glu Pro Asp Lys Gln Lys Leu Phe Glu Thr Ile Ser Phe Glu Glu
195 200 205

Leu His Lys Glu Ile Ile Glu Leu Arg Glu Phe Thr Gly Leu Leu Asn
210 215 220

Ala Pro Val Val Phe Ala His Asn Asp Leu Leu Ser Gly Asn Phe Met
225 230 235 240

Leu Asn Asp Glu Glu Lys Leu Tyr Leu Ile Asp Phe Glu Tyr Gly
245 250 255

Ser Tyr Asn Tyr Arg Gly Phe Asp Ile Gly Asn His Phe Asn Glu Tyr
260 265 270

Ala Gly Tyr Asp Cys Asp Tyr Ser Leu Tyr Pro Ser Lys Glu Glu Gln
 275 280 285

Tyr His Phe Ile Lys His Tyr Leu Gln Pro Asp Lys Pro Asp Glu Val
 290 295 300

Ser Ile Ala Glu Val Glu Ser Val Phe Val Glu Thr Asp Ala Tyr Lys
 305 310 315 320

Leu Ala Ser His Leu Tyr Trp Ala Ile Trp Ala Ile Ile Gln Ala Arg
 325 330 335

Met Ser Pro Ile Glu Phe Glu Tyr Leu Gly Tyr Phe Phe Leu Arg Tyr
 340 345 350

Asn Glu Tyr Lys Lys Gln Lys Pro Leu Thr Phe Ser Leu Val Thr Ser
 355 360 365

His Leu Ser Ala Ser Leu
 370

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<211> 2283

<212> DNA

<213> *Arabidopsis thaliana*

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<221> CDS

<222> (1)..(2283)

<223> 13823

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 Met Ala Met Thr Pro Val Ala Ser Ser Ser Pro Val Ser Thr Cys Arg
 1 5 10 15

ctc ttt cgc tgc aat ctc ctc cct gat ctc tta cct aag cct ctg ttt 96
 Leu Phe Arg Cys Asn Leu Leu Pro Asp Leu Leu Pro Lys Pro Leu Phe
 20 25 30

ctc tcc ctc ccc aaa cga aac aga att gcc tcg tgc cgc ttc act gta 144

Leu Ser Leu Pro Lys Arg Asn Arg Ile Ala Ser Cys Arg Phe Thr Val		
35	40	45
cgt gcc tcc gcg aat gct acc gtc gaa tcc cct aac ggt gtc cct gcc		192
Arg Ala Ser Ala Asn Ala Thr Val Glu Ser Pro Asn Gly Val Pro Ala		
50	55	60
tcc aca tca gat acg gat acg gag acg gat acc acc tcc tat ggc cga		240
Ser Thr Ser Asp Thr Asp Thr Glu Thr Asp Thr Ser Tyr Gly Arg		
65	70	75
cag ttt ttc cct ttg gcc gca gtt gtt ggc cag gaa ggc ata aaa act		288
Gln Phe Phe Pro Leu Ala Ala Val Val Gly Gln Glu Gly Ile Lys Thr		
85	90	95
gct ctt tta ctt ggc gcg gtt gat cgt gaa atc gga ggg att gcc att		336
Ala Leu Leu Leu Gly Ala Val Asp Arg Glu Ile Gly Gly Ile Ala Ile		
100	105	110
tca ggt cgt aga ggc act gca aaa aca gtc atg gcg cga ggg ctt cat		384
Ser Gly Arg Arg Gly Thr Ala Lys Thr Val Met Ala Arg Gly Leu His		
115	120	125
gaa atc ctc cct cct att gaa gtt gtt gta ggc tca ata tca aat gct		432
Glu Ile Leu Pro Pro Ile Glu Val Val Val Gly Ser Ile Ser Asn Ala		
130	135	140
gac cca gct tgt cca gat gag tgg gaa gat gac tta gat gag cgc ata		480
Asp Pro Ala Cys Pro Asp Glu Trp Glu Asp Asp Leu Asp Glu Arg Ile		
145	150	155
160		
gag tac aat gct gac aat acc att aag act gag att gtc aaa tct cct		528
Glu Tyr Asn Ala Asp Asn Thr Ile Lys Thr Glu Ile Val Lys Ser Pro		
165	170	175
ttc att cag att cca cta gga gtt aca gaa gac aga ctc att ggg tct		576
Phe Ile Gln Ile Pro Leu Gly Val Thr Glu Asp Arg Leu Ile Gly Ser		
180	185	190
gtt gat gtt gag gag tct gtg aaa agg ggg aca act gtt ttc caa cct		624
Val Asp Val Glu Glu Ser Val Lys Arg Gly Thr Thr Val Phe Gln Pro		
195	200	205
ggt ctt ttg gct gaa gcc cat aga gga gtg ttg tat gtt gat gaa ata		672
Gly Leu Leu Ala Glu Ala His Arg Gly Val Leu Tyr Val Asp Glu Ile		
210	215	220
aat ctc tta gat gag gga att agt aat ttg ctt ctc aat gta ttg acg		720
Asn Leu Leu Asp Glu Gly Ile Ser Asn Leu Leu Asn Val Leu Thr		
225	230	235
240		
gat ggt gtt aat ata gtt gaa aga gaa gga atc agc ttt agg cac ccg		768
Asp Gly Val Asn Ile Val Glu Arg Glu Gly Ile Ser Phe Arg His Pro		
245	250	255
tgc aaa cca ctt tta att gca acc tat aac cct gaa gaa ggt gct gtt		816
Cys Lys Pro Leu Leu Ile Ala Thr Tyr Asn Pro Glu Glu Gly Ala Val		
260	265	270
cga gag cac ttg cta gac cgt gtt gcc att aat tta agt gca gac cta		864

Arg Glu His Leu Leu Asp Arg Val Ala Ile Asn Leu Ser Ala Asp Leu			
275	280	285	
cct atg agt ttt gaa gat cgt gtc gca gca gtt gga att gcc aca cag			912
Pro Met Ser Phe Glu Asp Arg Val Ala Ala Val Gly Ile Ala Thr Gln			
290	295	300	
ttt cag gaa cgc tgt aat gag gtt ttt aga atg gta aat gaa gag aca			960
Phe Gln Glu Arg Cys Asn Glu Val Phe Arg Met Val Asn Glu Glu Thr			
305	310	315	320
gaa aca gca aag acg cag att ata ttg gct aga gaa tat ttg aaa gat			1008
Glu Thr Ala Lys Thr Gln Ile Ile Leu Ala Arg Glu Tyr Leu Lys Asp			
325	330	335	
gtc aag ata agt aga gag caa ttg aag tat ctg gtt ttg gaa gct gtc			1056
Val Lys Ile Ser Arg Glu Gln Leu Lys Tyr Leu Val Leu Glu Ala Val			
340	345	350	
cga ggt ggt gtc cag gga cac cgc gcc gaa ttg tat gca gct cgt gtg			1104
Arg Gly Gly Val Gln Gly His Arg Ala Glu Leu Tyr Ala Ala Arg Val			
355	360	365	
gcg aag tgt tta gct gca att gaa gga cga gaa aaa gtc aca atc gat			1152
Ala Lys Cys Leu Ala Ala Ile Glu Gly Arg Glu Lys Val Thr Ile Asp			
370	375	380	
gac ctc aga aag gcc gtt gag ctg gtc att ctt cct cgt tca tca cta			1200
Asp Leu Arg Lys Ala Val Glu Leu Val Ile Leu Pro Arg Ser Ser Leu			
385	390	395	400
gat gag act cca cct gaa caa caa aac caa cca cca cct cct cca cct			1248
Asp Glu Thr Pro Pro Glu Gln Gln Asn Gln Pro Pro Pro Pro Pro			
405	410	415	
cct cca caa aat agc gaa tct gga gaa gaa aat gaa gaa gaa caa			1296
Pro Pro Gln Asn Ser Glu Ser Gly Glu Glu Asn Glu Glu Glu Gln			
420	425	430	
gaa gaa gaa gag gat gaa agc aat gaa gaa aat gaa aat gag cag			1344
Glu Glu Glu Glu Asp Glu Ser Asn Glu Glu Asn Glu Asn Glu Gln			
435	440	445	
caa cag gac caa ata cct gaa gag ttt ata ttt gac gct gag ggc ggt			1392
Gln Gln Asp Gln Ile Pro Glu Glu Phe Ile Phe Asp Ala Glu Gly Gly			
450	455	460	
ctg gtg gat gag aaa ctc ctc ttc ttt gct caa caa gcc cag aaa cgt			1440
Leu Val Asp Glu Lys Leu Leu Phe Phe Ala Gln Gln Ala Gln Lys Arg			
465	470	475	480
cgg ggg aaa gct ggc agg gcg aag aat gtc ata ttc tca gaa gat aga			1488
Arg Gly Lys Ala Gly Arg Ala Lys Asn Val Ile Phe Ser Glu Asp Arg			
485	490	495	
gga cgc tac ata aag cca atg ctt cca aag ggt cca gta aaa aga tta			1536
Gly Arg Tyr Ile Lys Pro Met Leu Pro Lys Gly Pro Val Lys Arg Leu			
500	505	510	
gct gtg gat gca acc ctt aga gca gct gca cca tac cag aaa ttg cgc			1584

Ala Val Asp Ala Thr Leu Arg Ala Ala Ala Pro Tyr Gln Lys Leu Arg			
515	520	525	
aga gag aag gat atc tca gga act agg aaa gtc ttt gtt gag aag aca		1632	
Arg Glu Lys Asp Ile Ser Gly Thr Arg Lys Val Phe Val Glu Lys Thr			
530	535	540	
gat atg agg gcc aaa aga atg gca agg aaa gct gga gcc ctg gtt atc		1680	
Asp Met Arg Ala Lys Arg Met Ala Arg Lys Ala Gly Ala Leu Val Ile			
545	550	555	560
ttt gtg gtt gat gca agt ggc agt atg gca ttg aat cgt atg caa aac		1728	
Phe Val Val Asp Ala Ser Gly Ser Met Ala Leu Asn Arg Met Gln Asn			
565	570	575	
gcc aaa ggt gct gca ctc aaa cta ctg gca gag agc tat act agc agg		1776	
Ala Lys Gly Ala Ala Leu Lys Leu Leu Ala Glu Ser Tyr Thr Ser Arg			
580	585	590	
gat cag gtt tcg att att cct ttc cga ggg gat gct gcg gaa gtg ctc		1824	
Asp Gln Val Ser Ile Ile Pro Phe Arg Gly Asp Ala Ala Glu Val Leu			
595	600	605	
ttg ccc cct tct aga tca ata gca atg gca agg aat cgt ctt gag aga		1872	
Leu Pro Pro Ser Arg Ser Ile Ala Met Ala Arg Asn Arg Leu Glu Arg			
610	615	620	
ctt cct tgt ggt ggt tct cct ctt gcc cat ggt tta aca acg gct		1920	
Leu Pro Cys Gly Gly Ser Pro Leu Ala His Gly Leu Thr Thr Ala			
625	630	635	640
gta aga gta gga ctt aac gca gag aag agt ggt gat gtc ggg cgc ata		1968	
Val Arg Val Gly Leu Asn Ala Glu Lys Ser Gly Asp Val Gly Arg Ile			
645	650	655	
atg att gtt gcg ata acc gat ggt cga gcc aac att aca ctg aaa aga		2016	
Met Ile Val Ala Ile Thr Asp Gly Arg Ala Asn Ile Thr Leu Lys Arg			
660	665	670	
tca act gat ccg gag tct att gcc cca gat gct cct aga ccc acg tcc		2064	
Ser Thr Asp Pro Glu Ser Ile Ala Pro Asp Ala Pro Arg Pro Thr Ser			
675	680	685	
aaa gaa ttg aag gat gag att ctg gaa gtt gct ggg aag ata tac aag		2112	
Lys Glu Leu Lys Asp Glu Ile Leu Glu Val Ala Gly Lys Ile Tyr Lys			
690	695	700	
gca ggg atg tct ctt cta gtg att gat acc gag aac aag ttt gtt tca		2160	
Ala Gly Met Ser Leu Leu Val Ile Asp Thr Glu Asn Lys Phe Val Ser			
705	710	715	720
act ggt ttt gca aag gag atc gca aga gtt gct caa gga aaa tat tat		2208	
Thr Gly Phe Ala Lys Glu Ile Ala Arg Val Ala Gln Gly Lys Tyr Tyr			
725	730	735	
tac ttg cca aat gct tcg gat gct gta atc tcg gcc acc act agg gat		2256	
Tyr Leu Pro Asn Ala Ser Asp Ala Val Ile Ser Ala Thr Thr Arg Asp			
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gca cta tct gat ctg aag aat tct tga		2283	

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20 25 30

Leu Ser Leu Pro Lys Arg Asn Arg Ile Ala Ser Cys Arg Phe Thr Val
35 40 45

Arg Ala Ser Ala Asn Ala Thr Val Glu Ser Pro Asn Gly Val Pro Ala
50 55 60

Ser Thr Ser Asp Thr Asp Thr Glu Thr Asp Thr Thr Ser Tyr Gly Arg
65 70 75 80

Gln Phe Phe Pro Leu Ala Ala Val Val Gly Gln Glu Gly Ile Lys Thr
85 90 95

Ala Leu Leu Leu Gly Ala Val Asp Arg Glu Ile Gly Gly Ile Ala Ile
100 105 110

Ser Gly Arg Arg Gly Thr Ala Lys Thr Val Met Ala Arg Gly Leu His
115 120 125

Glu Ile Leu Pro Pro Ile Glu Val Val Val Gly Ser Ile Ser Asn Ala
130 135 140

Asp Pro Ala Cys Pro Asp Glu Trp Glu Asp Asp Leu Asp Glu Arg Ile
145 150 155 160

Glu Tyr Asn Ala Asp Asn Thr Ile Lys Thr Glu Ile Val Lys Ser Pro
165 170 175

Phe Ile Gln Ile Pro Leu Gly Val Thr Glu Asp Arg Leu Ile Gly Ser
180 185 190

Val Asp Val Glu Glu Ser Val Lys Arg Gly Thr Thr Val Phe Gln Pro
195 200 205

Gly Leu Leu Ala Glu Ala His Arg Gly Val Leu Tyr Val Asp Glu Ile
210 215 220

Asn Leu Leu Asp Glu Gly Ile Ser Asn Leu Leu Asn Val Leu Thr
225 230 235 240

Asp Gly Val Asn Ile Val Glu Arg Glu Gly Ile Ser Phe Arg His Pro
245 250 255

Cys Lys Pro Leu Leu Ile Ala Thr Tyr Asn Pro Glu Glu Gly Ala Val
260 265 270

Arg Glu His Leu Leu Asp Arg Val Ala Ile Asn Leu Ser Ala Asp Leu
275 280 285

Pro Met Ser Phe Glu Asp Arg Val Ala Ala Val Gly Ile Ala Thr Gln
290 295 300

Phe Gln Glu Arg Cys Asn Glu Val Phe Arg Met Val Asn Glu Glu Thr
305 310 315 320

Glu Thr Ala Lys Thr Gln Ile Ile Leu Ala Arg Glu Tyr Leu Lys Asp
325 330 335

Val Lys Ile Ser Arg Glu Gln Leu Lys Tyr Leu Val Leu Glu Ala Val
340 345 350

Arg Gly Gly Val Gln Gly His Arg Ala Glu Leu Tyr Ala Ala Arg Val
355 360 365

Ala Lys Cys Leu Ala Ala Ile Glu Gly Arg Glu Lys Val Thr Ile Asp
370 375 380

Asp Leu Arg Lys Ala Val Glu Leu Val Ile Leu Pro Arg Ser Ser Leu
385 390 395 400

Asp Glu Thr Pro Pro Glu Gln Gln Asn Gln Pro Pro Pro Pro Pro
405 410 415

Pro Pro Gln Asn Ser Glu Ser Gly Glu Glu Glu Asn Glu Glu Glu Gln
420 425 430

Glu Glu Glu Glu Glu Asp Glu Ser Asn Glu Glu Asn Glu Asn Glu Gln
435 440 445

Gln Gln Asp Gln Ile Pro Glu Glu Phe Ile Phe Asp Ala Glu Gly Gly
450 455 460

Leu Val Asp Glu Lys Leu Leu Phe Phe Ala Gln Gln Ala Gln Lys Arg
465 470 475 480

Arg Gly Lys Ala Gly Arg Ala Lys Asn Val Ile Phe Ser Glu Asp Arg
485 490 495

Gly Arg Tyr Ile Lys Pro Met Leu Pro Lys Gly Pro Val Lys Arg Leu
500 505 510

Ala Val Asp Ala Thr Leu Arg Ala Ala Ala Pro Tyr Gln Lys Leu Arg
515 520 525

Arg Glu Lys Asp Ile Ser Gly Thr Arg Lys Val Phe Val Glu Lys Thr
530 535 540

Asp Met Arg Ala Lys Arg Met Ala Arg Lys Ala Gly Ala Leu Val Ile
545 550 555 560

Phe Val Val Asp Ala Ser Gly Ser Met Ala Leu Asn Arg Met Gln Asn
565 570 575

Ala Lys Gly Ala Ala Leu Lys Leu Leu Ala Glu Ser Tyr Thr Ser Arg
580 585 590

Asp Gln Val Ser Ile Ile Pro Phe Arg Gly Asp Ala Ala Glu Val Leu
595 600 605

Leu Pro Pro Ser Arg Ser Ile Ala Met Ala Arg Asn Arg Leu Glu Arg
610 615 620

Leu Pro Cys Gly Gly Ser Pro Leu Ala His Gly Leu Thr Thr Ala
625 630 635 640

Val Arg Val Gly Leu Asn Ala Glu Lys Ser Gly Asp Val Gly Arg Ile
645 650 655

Met Ile Val Ala Ile Thr Asp Gly Arg Ala Asn Ile Thr Leu Lys Arg
 660 665 670

Ser Thr Asp Pro Glu Ser Ile Ala Pro Asp Ala Pro Arg Pro Thr Ser
 675 680 685

Lys Glu Leu Lys Asp Glu Ile Leu Glu Val Ala Gly Lys Ile Tyr Lys
 690 695 700

Ala Gly Met Ser Leu Leu Val Ile Asp Thr Glu Asn Lys Phe Val Ser
 705 710 715 720

Thr Gly Phe Ala Lys Glu Ile Ala Arg Val Ala Gln Gly Lys Tyr Tyr
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 1 5 10 15

att gct tca ttc act gga aat gga gaa gct tct tct tcc tca gag 96
 Ile Ala Ser Phe Thr Gly Asn Gly Glu Ala Ser Ser Ser Ser Glu
 20 25 30

aac aat ggc tgc aat gga gat caa aac cat ttg ctt aac gaa ctc aaa 144
 Asn Asn Gly Cys Asn Gly Asp Gln Asn His Leu Leu Asn Glu Leu Lys
 35 40 45

tcc acc gtc tct gct ctt caa tca atc atc aag gag aaa aac caa gaa	50	55	60	192
Ser Thr Val Ser Ala Leu Gln Ser Ile Ile Lys Glu Lys Asn Gln Glu				
ttg ctt agc aag gaa gag aaa atc cga ggt ttg gag tta tat atc agg	65	70	75	240
Leu Leu Ser Lys Glu Glu Lys Ile Arg Gly Leu Glu Leu Tyr Ile Arg				
gag aaa cct tat ttg ttt gag agt gaa att gat ttt tct caa ttt gag	85	90	95	288
Glu Lys Pro Tyr Leu Phe Glu Ser Glu Ile Asp Phe Ser Gln Phe Glu				
aat ccg gta aag cat gcg agt gaa gta gaa gag aag gtt tat gaa cta	100	105	110	336
Asn Pro Val Lys His Ala Ser Glu Val Glu Glu Lys Val Tyr Glu Leu				
cag aaa cag gta ttt gga tta aaa cgg gaa gtt gaa acg caa cgc aag	115	120	125	384
Gln Lys Gln Val Phe Gly Leu Lys Arg Glu Val Glu Thr Gln Arg Lys				
aga agg ctc gaa gtt gaa gct gaa tta gca gat aag aaa gtt gca caa	130	135	140	432
Arg Arg Leu Glu Val Glu Ala Glu Leu Ala Asp Lys Lys Val Ala Gln				
ctt agc tca aag ctt gaa aat atc gat ggg tgg ttc ttg tct aaa ctt	145	150	155	480
Leu Ser Ser Lys Leu Glu Asn Ile Asp Gly Trp Phe Leu Ser Lys Leu				
ggt ctt aac ccg act gaa agt cag gca tat ctg atg acc cta tgg cat	165	170	175	528
Gly Leu Asn Pro Thr Glu Ser Gln Ala Tyr Leu Met Thr Leu Trp His				
caa cat ctt agc cca act ctt cat acc act ctt caa atg gtt tcg atg	180	185	190	576
Gln His Leu Ser Pro Thr Leu His Thr Thr Leu Gln Met Val Ser Met				
aaa att gag caa gtc cag aaa tgg tca gag ctt cac att gaa aca ctg	195	200	205	624
Lys Ile Glu Gln Val Gln Lys Trp Ser Glu Pro His Ile Glu Thr Leu				
aac tca caa tgg att cca agc atc aaa gat gca tgt gtc aca ata acc	210	215	220	672
Asn Ser Gln Trp Ile Pro Ser Ile Lys Asp Ala Cys Val Thr Ile Thr				
ata tat ctc gaa cca aaa gtt caa tat ata acc gat aag tcc atc gag	225	230	235	720
Ile Tyr Leu Glu Pro Lys Val Gln Tyr Ile Thr Asp Lys Ser Ile Glu				
ttg tta tat aca tct aag cag gct ttg aca cca cat ctc atc caa gga	245	250	255	768
Leu Leu Tyr Thr Ser Lys Gln Ala Leu Thr Pro His Leu Ile Gln Gly				
ttt gac gct tca tac tac tat ctt gag gtt atc aga aca cat aca cat	260	265	270	816
Phe Asp Ala Ser Tyr Tyr Leu Glu Val Ile Arg Thr His Thr His				
ccg tac acg acc cgg att atg acc tta acg aag cca cac ttg gag aga	275	280	285	864
Pro Tyr Thr Thr Arg Ile Met Thr Leu Thr Lys Pro His Leu Glu Arg				

gta caa gtt gcc tta gag cca tat act gaa aac gta aga cat ggc ttt	912
Val Gln Val Ala Leu Glu Pro Tyr Thr Glu Asn Val Arg His Gly Phe	
290 295 300	
cag aag ttg gtt aac tca acc aaa atc tac cat caa cag gct caa gaa	960
Gln Lys Leu Val Asn Ser Thr Lys Ile Tyr His Gln Gln Ala Gln Glu	
305 310 315 320	
atg ctg aag aac aat gag atc acc aaa ccg gtt gct acc atg gac tta	1008
Met Leu Lys Asn Asn Glu Ile Thr Lys Pro Val Ala Thr Met Asp Leu	
325 330 335	
gct tgg gtt ggg gcc aca gct tta att gga ttc cct ctt ata ttc atc	1056
Ala Trp Val Gly Ala Thr Ala Leu Ile Gly Phe Pro Leu Ile Phe Ile	
340 345 350	
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Ile Lys Leu Leu Ser Ala Val Ser Asn Pro Lys Gly Lys Lys Arg His	
355 360 365	
aac cat aaa aaa gaa cca acc acc ggg tac cgc aga gcc aaa cgc cga	1152
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Ser Thr Val Ser Ala Leu Gln Ser Ile Ile Lys Glu Lys Asn Gln Glu	
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Leu Leu Ser Lys Glu Glu Lys Ile Arg Gly Leu Glu Leu Tyr Ile Arg	
65 70 75 80	

Glu Lys Pro Tyr Leu Phe Glu Ser Glu Ile Asp Phe Ser Gln Phe Glu
85 90 95

Asn Pro Val Lys His Ala Ser Glu Val Glu Glu Lys Val Tyr Glu Leu
100 105 110

Gln Lys Gln Val Phe Gly Leu Lys Arg Glu Val Glu Thr Gln Arg Lys
115 120 125

Arg Arg Leu Glu Val Glu Ala Glu Leu Ala Asp Lys Lys Val Ala Gln
130 135 140

Leu Ser Ser Lys Leu Glu Asn Ile Asp Gly Trp Phe Leu Ser Lys Leu
145 150 155 160

Gly Leu Asn Pro Thr Glu Ser Gln Ala Tyr Leu Met Thr Leu Trp His
165 170 175

Gln His Leu Ser Pro Thr Leu His Thr Thr Leu Gln Met Val Ser Met
180 185 190

Lys Ile Glu Gln Val Gln Lys Trp Ser Glu Pro His Ile Glu Thr Leu
195 200 205

Asn Ser Gln Trp Ile Pro Ser Ile Lys Asp Ala Cys Val Thr Ile Thr
210 215 220

Ile Tyr Leu Glu Pro Lys Val Gln Tyr Ile Thr Asp Lys Ser Ile Glu
225 230 235 240

Leu Leu Tyr Thr Ser Lys Gln Ala Leu Thr Pro His Leu Ile Gln Gly
245 250 255

Phe Asp Ala Ser Tyr Tyr Tyr Leu Glu Val Ile Arg Thr His Thr His
260 265 270

Pro Tyr Thr Thr Arg Ile Met Thr Leu Thr Lys Pro His Leu Glu Arg
275 280 285

Val Gln Val Ala Leu Glu Pro Tyr Thr Glu Asn Val Arg His Gly Phe
290 295 300

Gln Lys Leu Val Asn Ser Thr Lys Ile Tyr His Gln Gln Ala Gln Glu
305 310 315 320

Met Leu Lys Asn Asn Glu Ile Thr Lys Pro Val Ala Thr Met Asp Leu
 325 330 335

Ala Trp Val Gly Ala Thr Ala Leu Ile Gly Phe Pro Leu Ile Phe Ile
 340 345 350

Ile Lys Leu Leu Ser Ala Val Ser Asn Pro Lys Gly Lys Lys Arg His
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Asn His Lys Lys Glu Pro Thr Thr Gly Tyr Arg Arg Ala Lys Arg Arg
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His Pro His Gln
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 Asn Arg Arg Tyr Leu Ser Gln Val Met Asp Thr Cys Gly Lys Asp Leu
 20 25 30

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 Ser Thr Ala Glu Asp Ile Val Asp Asp Leu Arg Ser Arg Tyr Gly Asn
 35 40 45

ttt gcg agg ttg act cgg caa gtg ctt cta ctc aat gtc agg caa gtc 192
 Phe Ala Arg Leu Thr Arg Gln Val Leu Leu Asn Val Arg Gln Val
 50 55 60

ctt aat gtt aga aac aac aag agg gtt aaa gac gaa gat gaa gat gac 240

Leu Asn Val Arg Asn Asn Lys Arg Val Lys Asp Glu Asp Glu Asp Asp			
65	70	75	80
aac att gga gat gag gaa ggt tct gct tct cag agg aag aaa cag aga			288
Asn Ile Gly Asp Glu Glu Gly Ser Ala Ser Gln Arg Lys Lys Gln Arg			
85	90	95	
cgg gtt gat gag aaa gag gag aaa ttg cag cga gcg gag cag tcg cat			336
Arg Val Asp Glu Lys Glu Lys Leu Gln Arg Ala Glu Gln Ser His			
100	105	110	
tta agg aag agg aat atg gaa cgt tca gtg tct tct tct ccg tct tct			384
Leu Arg Lys Arg Asn Met Glu Arg Ser Val Ser Ser Pro Ser Ser			
115	120	125	
tct tct tct tcg gaa gac agt ggt gat gtg tcg act tct gag gac gcg			432
Ser Ser Ser Glu Asp Ser Gly Asp Val Ser Thr Ser Glu Asp Ala			
130	135	140	
gtt tat ggc gag aag ctg agt ccg ccg cgg ttt gat ctg atc aat gac			480
Val Tyr Gly Glu Lys Leu Ser Pro Pro Arg Phe Asp Leu Ile Asn Asp			
145	150	155	160
agt cta aga gat aac tac gct aag ttg aac agc tcc tcg aag aaa cca			528
Ser Leu Arg Asp Asn Tyr Ala Lys Leu Asn Ser Ser Ser Lys Lys Pro			
165	170	175	
att ggg tcg cct gcg gaa aag aat gtg gaa gtt gag act gtg agc aac			576
Ile Gly Ser Pro Ala Glu Lys Asn Val Glu Val Glu Thr Val Ser Asn			
180	185	190	
aaa ggt aga agc aag ttg gct aca atg ggg gcc aga aag gag gct aaa			624
Lys Gly Arg Ser Lys Leu Ala Thr Met Gly Ala Arg Lys Glu Ala Lys			
195	200	205	
gtt tct ctt tcc ctc agt gga gct act ggt aat ggt gat ttg gaa gtt			672
Val Ser Leu Ser Leu Ser Gly Ala Thr Gly Asn Gly Asp Leu Glu Val			
210	215	220	
gag ggt act aaa gga cct act ttt aaa gac ttt ggt ggg att aag aaa			720
Glu Gly Thr Lys Gly Pro Thr Phe Lys Asp Phe Gly Gly Ile Lys Lys			
225	230	235	240
ata ttg gat gaa ttg gag atg aat gtt cta ttc ccc att ctc aat cct			768
Ile Leu Asp Glu Leu Glu Met Asn Val Leu Phe Pro Ile Leu Asn Pro			
245	250	255	
gag ccg ttt aag aag att gga gtg aag cca cca agt ggg att cta ttt			816
Glu Pro Phe Lys Lys Ile Gly Val Lys Pro Pro Ser Gly Ile Leu Phe			
260	265	270	
cat gga cca cct ggc tgt ggg aag act aag ttg gcc aat gcc att gcc			864
His Gly Pro Pro Gly Cys Gly Lys Thr Lys Leu Ala Asn Ala Ile Ala			
275	280	285	
aat gaa gct ggt gtt ccg ttt tat aag att tca gcc aca gag gtg att			912
Asn Glu Ala Gly Val Pro Phe Tyr Lys Ile Ser Ala Thr Glu Val Ile			
290	295	300	
tct ggt gtt tct ggt gct tct gaa gag aat atc aga gag ctc ttt tct			960

Ser	Gly	Val	Ser	Gly	Ala	Ser	Glu	Glu	Asn	Ile	Arg	Glu	Leu	Phe	Ser	
305							310				315				320	
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Lys	Ala	Tyr	Arg	Thr	Ala	Pro	Ser	Ile	Val	Phe	Ile	Asp	Glu	Ile	Asp	
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gcg att ggt tca aag aga gag aat cag caa aga gag atg gag aag cgg															1056	
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							340			345			350			
ata gta aca caa ttg ttg act tgt atg gat gga cct ggt aac aaa ggc															1104	
Ile	Val	Thr	Gln	Leu	Leu	Thr	Cys	Met	Asp	Gly	Pro	Gly	Asn	Lys	Gly	
							355			360			365			
gat aaa aat gct cct gat tct agt gct ggt ttt gtt ctt gtc att gga															1152	
Asp	Lys	Asn	Ala	Pro	Asp	Ser	Ser	Ala	Gly	Phe	Val	Leu	Val	Ile	Gly	
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Ala	Thr	Asn	Arg	Pro	Asp	Ala	Leu	Asp	Pro	Ala	Leu	Arg	Arg	Ser	Gly	
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cga ttt gaa act gag atc gct cta act gct cca gat gaa gac gca agg															1248	
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							420			425			430			
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Phe	Asp	Lys	Arg	Ile	Ala	Arg	Leu	Thr	Pro	Gly	Phe	Val	Gly	Ala		
							435			440			445			
gat ttg gag agt gtt gct tac ttg gct ggc agg aaa gcc att aag aga															1392	
Asp	Leu	Glu	Ser	Val	Ala	Tyr	Leu	Ala	Gly	Arg	Lys	Ala	Ile	Lys	Arg	
							450			455			460			
atc ttg gat tca agg aaa tct gaa cag tct ggg gac ggt gaa gac gat															1440	
Ile	Leu	Asp	Ser	Arg	Lys	Ser	Glu	Gln	Ser	Gly	Asp	Gly	Glu	Asp	Asp	
							465			470			475		480	
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							485			490			495			
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Phe	Val	Lys	Met	Ser	Asp	Phe	Glu	Glu	Ala	Val	Asn	Leu	Val	Gln	Ala	
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Ser	Leu	Thr	Arg	Glu	Gly	Phe	Ser	Ile	Val	Pro	Asp	Val	Lys	Trp	Asp	
							515			520			525			
gat gtt ggt gga ctt gac cat cta cga ctt caa ttc aac cgt tat ata															1632	
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Val	Arg	Pro	Ile	Lys	Lys	Pro	Asp	Ile	Tyr	Lys	Ala	Phe	Gly	Val	Asp	
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Leu Glu Thr Gly Phe Leu Leu Tyr Gly Pro Pro Gly Cys Gly Lys Thr																
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Leu Ile Ala Lys Ala Ala Asn Glu Ala Gly Ala Asn Phe Met His																
580 585 590																
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Ile Lys Gly Ala Glu Leu Leu Asn Lys Tyr Val Gly Glu Ser Glu Leu																
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Gly Ala Trp Val Val Glu Arg Leu Leu Asn Gln Phe Leu Val Glu Leu																
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740 745 750																
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Ser Ser Glu Ser Ser Glu Asp Asp Val Thr Asp Ile Thr Gln Cys Thr																
755 760 765																
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Ile Lys Thr Arg His Phe Glu Gln Ala Leu Ser Leu Val Ser Pro Ser																
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785	790	795	800
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Phe Thr Leu Glu			
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35	40	45	
Phe Ala Arg Leu Thr Arg Gln Val Leu Leu Leu Asn Val Arg Gln Val			
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Leu Asn Val Arg Asn Asn Lys Arg Val Lys Asp Glu Asp Glu Asp Asp			
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Asn Ile Gly Asp Glu Glu Gly Ser Ala Ser Gln Arg Lys Lys Gln Arg			
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Arg Val Asp Glu Lys Glu Glu Lys Leu Gln Arg Ala Glu Gln Ser His			
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Leu Arg Lys Arg Asn Met Glu Arg Ser Val Ser Ser Ser Pro Ser Ser			
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Val Tyr Gly Glu Lys Leu Ser Pro Pro Arg Phe Asp Leu Ile Asn Asp
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Ser Leu Arg Asp Asn Tyr Ala Lys Leu Asn Ser Ser Ser Lys Lys Pro
165 170 175

Ile Gly Ser Pro Ala Glu Lys Asn Val Glu Val Glu Thr Val Ser Asn
180 185 190

Lys Gly Arg Ser Lys Leu Ala Thr Met Gly Ala Arg Lys Glu Ala Lys
195 200 205

Val Ser Leu Ser Leu Ser Gly Ala Thr Gly Asn Gly Asp Leu Glu Val
210 215 220

Glu Gly Thr Lys Gly Pro Thr Phe Lys Asp Phe Gly Gly Ile Lys Lys
225 230 235 240

Ile Leu Asp Glu Leu Glu Met Asn Val Leu Phe Pro Ile Leu Asn Pro
245 250 255

Glu Pro Phe Lys Lys Ile Gly Val Lys Pro Pro Ser Gly Ile Leu Phe
260 265 270

His Gly Pro Pro Gly Cys Gly Lys Thr Lys Leu Ala Asn Ala Ile Ala
275 280 285

Asn Glu Ala Gly Val Pro Phe Tyr Lys Ile Ser Ala Thr Glu Val Ile
290 295 300

Ser Gly Val Ser Gly Ala Ser Glu Glu Asn Ile Arg Glu Leu Phe Ser
305 310 315 320

Lys Ala Tyr Arg Thr Ala Pro Ser Ile Val Phe Ile Asp Glu Ile Asp
325 330 335

Ala Ile Gly Ser Lys Arg Glu Asn Gln Gln Arg Glu Met Glu Lys Arg
340 345 350

Ile Val Thr Gln Leu Leu Thr Cys Met Asp Gly Pro Gly Asn Lys Gly
355 360 365

Asp Lys Asn Ala Pro Asp Ser Ser Ala Gly Phe Val Leu Val Ile Gly
370 375 380

Ala Thr Asn Arg Pro Asp Ala Leu Asp Pro Ala Leu Arg Arg Ser Gly
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Arg Phe Glu Thr Glu Ile Ala Leu Thr Ala Pro Asp Glu Asp Ala Arg
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Ala Glu Ile Leu Ser Val Val Ala Gln Lys Leu Arg Leu Glu Gly Pro
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Phe Asp Lys Lys Arg Ile Ala Arg Leu Thr Pro Gly Phe Val Gly Ala
435 440 445

Asp Leu Glu Ser Val Ala Tyr Leu Ala Gly Arg Lys Ala Ile Lys Arg
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Ile Leu Asp Ser Arg Lys Ser Glu Gln Ser Gly Asp Gly Glu Asp Asp
465 470 475 480

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485 490 495

Phe Val Lys Met Ser Asp Phe Glu Glu Ala Val Asn Leu Val Gln Ala
500 505 510

Ser Leu Thr Arg Glu Gly Phe Ser Ile Val Pro Asp Val Lys Trp Asp
515 520 525

Asp Val Gly Gly Leu Asp His Leu Arg Leu Gln Phe Asn Arg Tyr Ile
530 535 540

Val Arg Pro Ile Lys Lys Pro Asp Ile Tyr Lys Ala Phe Gly Val Asp
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565 570 575

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Ile Lys Gly Ala Glu Leu Leu Asn Lys Tyr Val Gly Glu Ser Glu Leu
595 600 605

Ala Ile Arg Thr Leu Phe Gln Arg Ala Arg Thr Cys Ala Pro Cys Val
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Gly Ala Trp Val Val Glu Arg Leu Leu Asn Gln Phe Leu Val Glu Leu
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Asp Gly Gly Glu Arg Arg Asn Val Tyr Val Ile Gly Ala Thr Asn Arg
660 665 670

Pro Asp Val Val Asp Pro Ala Phe Leu Arg Pro Gly Arg Phe Gly Asn
675 680 685

Leu Leu Tyr Val Pro Leu Pro Asn Ala Asp Glu Arg Ala Ser Ile Leu
690 695 700

Lys Ala Ile Ala Arg Lys Lys Pro Ile Asp Pro Ser Val Asp Leu Asp
705 710 715 720

Gly Ile Ala Lys Asn Asn Cys Glu Gly Phe Ser Gly Ala Asp Leu Ala
725 730 735

His Leu Val Gln Lys Ala Thr Phe Gln Ala Val Glu Glu Met Ile Gly
740 745 750

Ser Ser Glu Ser Ser Glu Asp Asp Val Thr Asp Ile Thr Gln Cys Thr
755 760 765

Ile Lys Thr Arg His Phe Glu Gln Ala Leu Ser Leu Val Ser Pro Ser
770 775 780

Val Asn Lys Gln Gln Arg Arg His Tyr Asp Ala Leu Ser Thr Lys Leu
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Ser Asn Ile Val Gly Ile Gln Glu Arg Lys Leu Pro Tyr Ile Val Ser				
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Arg Cys Pro Lys Ile Leu Thr Leu Arg Leu Asp Glu Arg Leu Ile Pro				
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Lys Leu Cys Pro Leu Leu Ala Phe Phe Gln Ala Leu Gly Val Pro Glu				
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Thr Gln Leu Gly Lys Met Ile Leu Phe Asn Pro Arg Leu Ile Ser Tyr				
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145 150 155 160				
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Gly Leu Asp Gln Asp Gly Met Ile Gly Lys Val Leu Val Lys Asn Pro				
165 170 175				
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 195 200 205

gtc atg aat ttc cca caa ctt ttg tgc aga gac gtt aac aag att ctc 672
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 210 215 220

aaa cca aat tat gat tat ttg aag gag tgt ggg ttt gga gat tcc cag 720
 Lys Pro Asn Tyr Asp Tyr Leu Lys Glu Cys Gly Phe Gly Asp Ser Gln
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ata gca acc atg gtc act ggt tat ccc caa atc ttg att aag agt gtt 768
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 245 250 255

aag aat tca cta cag cct agg atc aga ttc ctc gtc cag gtg atg gga 816
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 260 265 270

aga ggc atg gat gaa gtg gct tct tat cct gaa ttc ttt cac cat gga 864
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 275 280 285

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 290 295 300

att gac tgc agc ctt aga gaa atg ctg gac tgt aac aca aag aaa ttc 960
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Arg Cys Pro Lys Ile Leu Thr Leu Arg Leu Asp Glu Arg Leu Ile Pro
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145 150 155 160

Gly Leu Asp Gln Asp Gly Met Ile Gly Lys Val Leu Val Lys Asn Pro
165 170 175

Phe Leu Met Gly Tyr Ser Val Asp Lys Arg Leu Arg Pro Thr Thr Glu
180 185 190

Phe Leu Lys Ser Ser Val Gly Leu Ser Glu Asp Gly Ile Lys Ser Val
195 200 205

Val Met Asn Phe Pro Gln Leu Leu Cys Arg Asp Val Asn Lys Ile Leu
210 215 220

Lys Pro Asn Tyr Asp Tyr Leu Lys Glu Cys Gly Phe Gly Asp Ser Gln
225 230 235 240

Ile Ala Thr Met Val Thr Gly Tyr Pro Gln Ile Leu Ile Lys Ser Val
245 250 255

Lys Asn Ser Leu Gln Pro Arg Ile Arg Phe Leu Val Gln Val Met Gly
260 265 270

Arg Gly Met Asp Glu Val Ala Ser Tyr Pro Glu Phe Phe His His Gly
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 Thr His Arg Ile Tyr Lys His Glu Cys Cys Ile Ser Phe Asp Thr Pro
 20 25 30

aga tcc gaa gga gga ttg ttc gtt gat atg aat agt ttt ctt gct ttc 144
 Arg Ser Glu Gly Gly Leu Phe Val Asp Met Asn Ser Phe Leu Ala Phe
 35 40 45

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 Gly Lys Asp Tyr Val Ser Trp Asn Tyr Glu Lys Thr Gly Asn Pro Val
 50 55 60

tat ctt cat att aag cag act agg aag tct att ccc gag gat cgg cct 240
 Tyr Leu His Ile Lys Gln Thr Arg Lys Ser Ile Pro Glu Asp Arg Pro
 65 70 75 80

ctc aag aaa ccg act ctg ctc gct ata ggt gtt gat gga ggc ttt gat 288
 Leu Lys Pro Thr Leu Leu Ala Ile Gly Val Asp Gly Phe Asp
 85 90 95

aac aat gag cca gag tac gag gag tct tat agc ata gtc ata ctt ccg 336

Asn Asn Glu Pro Glu Tyr Glu Glu Ser Tyr Ser Ile Val Ile Leu Pro.			
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gat ttt gtt tca ctc ccg ttt cct tct gtt gag cta cca gag aag gtg			384
Asp Phe Val Ser Leu Pro Phe Pro Ser Val Glu Leu Pro Glu Lys Val			
115	120	125	
agg att gct gtc gat act gta gtg aat gcc gtt ggt gct gag cgg aaa			432
Arg Ile Ala Val Asp Thr Val Val Asn Ala Val Gly Ala Glu Arg Lys			
130	135	140	
gag caa gtt gca gct tgg aca gct gag aaa aag tta att agt gaa cat			480
Glu Gln Val Ala Ala Trp Thr Ala Glu Lys Lys Leu Ile Ser Glu His			
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gca ttg aca ctg cag caa atc aag agt ggc att gtc att cct ccc tct			528
Ala Leu Thr Leu Gln Gln Ile Lys Ser Gly Ile Val Ile Pro Pro Ser			
165	170	175	
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Gly Trp Lys Cys Ser Lys Cys Asp Lys Thr Glu Asn Leu Trp Leu Asn			
180	185	190	
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Leu Thr Asp Gly Met Ile Leu Cys Gly Arg Lys Asn Trp Asp Gly Thr			
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Gly Gly Asn Asn His Ala Val Glu His Tyr Lys Glu Thr Ala Tyr Pro			
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Leu Ala Val Lys Leu Gly Thr Ile Thr Ala Asp Leu Glu Ala Ala Asp			
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Val Tyr Ser Tyr Pro Glu Asp Asp Ser Val Leu Asp Pro Leu Leu Ala			
245	250	255	
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Glu His Leu Ala His Phe Gly Ile Asp Phe Ser Ser Met Gln Lys Thr			
260	265	270	
gaa atg aca act gct gaa aga gaa ctt gat caa aat aca aat ttt gat			864
Glu Met Thr Thr Ala Glu Arg Glu Leu Asp Gln Asn Thr Asn Phe Asp			
275	280	285	
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Trp Asn Arg Ile Gln Glu Ser Gly Lys Glu Leu Val Pro Val Phe Gly			
290	295	300	
cct gga tat acc gga ctt gtc aat ctt ggg aac agt tgc tac ttg gca			960
Pro Gly Tyr Thr Gly Leu Val Asn Leu Gly Asn Ser Cys Tyr Leu Ala			
305	310	315	320
gct acg atg cag att gtt ttc tct acc cat tca ttt att tca aga tac			1008
Ala Thr Met Gln Ile Val Phe Ser Thr His Ser Phe Ile Ser Arg Tyr			
325	330	335	
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Phe Ser His Gln Ser Leu Lys Met Ala Phe Glu Met Ala Pro Ala Asp			
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cca act ttg gac ctc aat atg caa tta aca aag ctt gga cac ggc tta			1104
Pro Thr Leu Asp Leu Asn Met Gln Leu Thr Lys Leu Gly His Gly Leu			
355	360	365	
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Leu Ser Gly Lys Tyr Ser Met Pro Ala Thr Gln Lys Asp Ala Thr Thr			
370	375	380	
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Gly Asp Pro Arg Gln Glu Gly Ile Pro Pro Arg Met Phe Lys Asn Val			
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Ile Ala Ala Ser His Ala Glu Phe Ser Ser Met Arg Gln Gln Asp Ala			
405	410	415	
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420	425	430	
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Thr Thr Pro Asp Leu Asp Pro Ser Arg Ser Phe Lys Phe Gly Ile Glu			
435	440	445	
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Glu Lys Ile Leu Cys Pro Ser Gly Lys Val Gly Tyr Asn Lys Arg Glu			
450	455	460	
gac tgt att ctt tct ttg aac att ccg cta cat gag gca act aat aaa			1440
Asp Cys Ile Leu Ser Leu Asn Ile Pro Leu His Glu Ala Thr Asn Lys			
465	470	475	480
gat gaa tta gaa gcc ttt cac aag caa aaa gca gga aaa gga ttg gaa			1488
Asp Glu Leu Glu Ala Phe His Lys Gln Lys Ala Gly Lys Gly Ile Glu			
485	490	495	
gag aat gat atg agg tca agt gat gaa ata gta cgc cca cga gtt cct			1536
Glu Asn Asp Met Arg Ser Ser Asp Glu Ile Val Arg Pro Arg Val Pro			
500	505	510	
tta gaa gcc tgt cta gca aat ttt gca tca tca gag ccg att gaa gac			1584
Leu Glu Ala Cys Leu Ala Asn Phe Ala Ser Ser Glu Pro Ile Glu Asp			
515	520	525	
tac tat agc tct gct ttg aag gga atg aca aca gct atc aag aca act			1632
Tyr Tyr Ser Ser Ala Leu Lys Gly Met Thr Thr Ala Ile Lys Thr Thr			
530	535	540	
ggt ttg aca tct ttc cca gat tat ttg gtc ttg cac atg cgg aaa ttt			1680
Gly Leu Thr Ser Phe Pro Asp Tyr Leu Val Leu His Met Arg Lys Phe			
545	550	555	560
gtt atg gag gaa ggc tgg gtg cca aag aaa ctt gat gta tac att gat			1728
Val Met Glu Glu Gly Trp Val Pro Lys Lys Leu Asp Val Tyr Ile Asp			
565	570	575	
gtt ccg gat gtt att gat atc agc cac atg cgt agc aaa gga ctc caa			1776

Val	Pro	Asp	Val	Ile	Asp	Ile	Ser	His	Met	Arg	Ser	Lys	Gly	Leu	Gln	
580								585						590		
cct ggg gaa gaa ctg ttg cca gat ggc gtt cca gaa gaa gtg atg gaa															1824	
Pro	Gly	Glu	Glu	Leu	Leu	Pro	Asp	Gly	Val	Pro	Glu	Val	Met	Glu		
595								600					605			
tca gcg cag ccc gtg gca aat gag gag ata gtt gca cag cta gtc tca															1872	
Ser	Ala	Gln	Pro	Val	Ala	Asn	Glu	Glu	Ile	Val	Ala	Gln	Leu	Val	Ser	
610								615					620			
atg gga ttt agc cag ctt cac tgc cag aaa gct gcc ata aat act tcc															1920	
Met	Gly	Phe	Ser	Gln	Leu	His	Cys	Gln	Lys	Ala	Ala	Ile	Asn	Thr	Ser	
625								630					635			
aat gct ggg gtt gaa gag gca atg aac tgg tta ctt tct cac atg gat															1968	
Asn	Ala	Gly	Val	Glu	Glu	Ala	Met	Asn	Trp	Leu	Leu	Ser	His	Met	Asp	
645								650					655			
gat cca gac atc gat gca cca atc tcc cac cag aca tct gac att gat															2016	
Asp	Pro	Asp	Ile	Asp	Ala	Pro	Ile	Ser	His	Gln	Thr	Ser	Asp	Ile	Asp	
660								665					670			
caa tca agc gtt gat acc tta ctc tcc ttt ggt ttt gct gaa gat gtt															2064	
Gln	Ser	Ser	Val	Asp	Thr	Leu	Leu	Ser	Phe	Gly	Phe	Ala	Glu	Asp	Val	
675								680					685			
gct cgg aag gca cta aaa gcc tcg gga gga gac att gag aaa gca aca															2112	
Ala	Arg	Lys	Ala	Leu	Lys	Ala	Ser	Gly	Gly	Asp	Ile	Glu	Lys	Ala	Thr	
690								695					700			
gac tgg gta ttc aac aac cct aat gca tct gtt tca gac atg gat gta															2160	
Asp	Trp	Val	Phe	Asn	Asn	Pro	Asn	Ala	Ser	Val	Ser	Asp	Met	Asp	Val	
705								710					715			
tcc tct agc aat tca gcg cag act ccg gct caa agt gga tta cca gat															2208	
Ser	Ser	Ser	Asn	Ser	Ala	Gln	Thr	Pro	Ala	Gln	Ser	Gly	Leu	Pro	Asp	
725								730					735			
gga gga ggg aaa tac aag ctg ttt gga ata gta agt cac atg gga aca															2256	
Gly	Gly	Gly	Tyr	Lys	Leu	Phe	Gly	Ile	Val	Ser	His	Met	Gly	Thr		
740								745					750			
tca gtg cac tgt ggt cat tac gtg gct cac ata ttg aaa gaa ggc cgc															2304	
Ser	Val	His	Cys	Gly	His	Tyr	Val	Ala	His	Ile	Leu	Lys	Glu	Gly	Arg	
755								760					765			
tgg gta att ttc aat gac gac aaa gtt ggt atc tcg act gat cct cct															2352	
Trp	Val	Ile	Phe	Asn	Asp	Asp	Lys	Val	Gly	Ile	Ser	Thr	Asp	Pro	Pro	
770								775					780			
aaa gac atg ggt tat gtc tac ttc ttt cag cgg ctt gat tga															2394	
Lys	Asp	Met	Gly	Tyr	Val	Tyr	Phe	Phe	Gln	Arg	Leu	Asp				
785								790					795			

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<211> 797

<212> PRT

<213> *Arabidopsis thaliana*

<400> 30

Met Glu Leu Leu Arg Ser Asn Leu Ser Arg Val Gln Ile Pro Glu Pro
1 5 10 15

Thr His Arg Ile Tyr Lys His Glu Cys Cys Ile Ser Phe Asp Thr Pro
20 25 30

Arg Ser Glu Gly Gly Leu Phe Val Asp Met Asn Ser Phe Leu Ala Phe
35 40 45

Gly Lys Asp Tyr Val Ser Trp Asn Tyr Glu Lys Thr Gly Asn Pro Val
50 55 60

Tyr Leu His Ile Lys Gln Thr Arg Lys Ser Ile Pro Glu Asp Arg Pro
65 70 75 80

Leu Lys Lys Pro Thr Leu Leu Ala Ile Gly Val Asp Gly Gly Phe Asp
85 90 95

Asn Asn Glu Pro Glu Tyr Glu Glu Ser Tyr Ser Ile Val Ile Leu Pro
100 105 110

Asp Phe Val Ser Leu Pro Phe Pro Ser Val Glu Leu Pro Glu Lys Val
115 120 125

Arg Ile Ala Val Asp Thr Val Val Asn Ala Val Gly Ala Glu Arg Lys
130 135 140

Glu Gln Val Ala Ala Trp Thr Ala Glu Lys Lys Leu Ile Ser Glu His
145 150 155 160

Ala Leu Thr Leu Gln Gln Ile Lys Ser Gly Ile Val Ile Pro Pro Ser
165 170 175

Gly Trp Lys Cys Ser Lys Cys Asp Lys Thr Glu Asn Leu Trp Leu Asn
180 185 190

Leu Thr Asp Gly Met Ile Leu Cys Gly Arg Lys Asn Trp Asp Gly Thr
195 200 205

Gly Gly Asn Asn His Ala Val Glu His Tyr Lys Glu Thr Ala Tyr Pro
210 215 220

Leu Ala Val Lys Leu Gly Thr Ile Thr Ala Asp Leu Glu Ala Ala Asp
225 230 235 240

Val Tyr Ser Tyr Pro Glu Asp Asp Ser Val Leu Asp Pro Leu Leu Ala
245 250 255

Glu His Leu Ala His Phe Gly Ile Asp Phe Ser Ser Met Gln Lys Thr
260 265 270

Glu Met Thr Thr Ala Glu Arg Glu Leu Asp Gln Asn Thr Asn Phe Asp
275 280 285

Trp Asn Arg Ile Gln Glu Ser Gly Lys Glu Leu Val Pro Val Phe Gly
290 295 300

Pro Gly Tyr Thr Gly Leu Val Asn Leu Gly Asn Ser Cys Tyr Leu Ala
305 310 315 320

Ala Thr Met Gln Ile Val Phe Ser Thr His Ser Phe Ile Ser Arg Tyr
325 330 335

Phe Ser His Gln Ser Leu Lys Met Ala Phe Glu Met Ala Pro Ala Asp
340 345 350

Pro Thr Leu Asp Leu Asn Met Gln Leu Thr Lys Leu Gly His Gly Leu
355 360 365

Leu Ser Gly Lys Tyr Ser Met Pro Ala Thr Gln Lys Asp Ala Thr Thr
370 375 380

Gly Asp Pro Arg Gln Glu Gly Ile Pro Pro Arg Met Phe Lys Asn Val
385 390 395 400

Ile Ala Ala Ser His Ala Glu Phe Ser Ser Met Arg Gln Gln Asp Ala
405 410 415

Leu Asp Phe Phe Leu His Leu Val Gly Lys Val Glu Arg Ala Ser Asn
420 425 430

Thr Thr Pro Asp Leu Asp Pro Ser Arg Ser Phe Lys Phe Gly Ile Glu
435 440 445

Glu Lys Ile Leu Cys Pro Ser Gly Lys Val Gly Tyr Asn Lys Arg Glu

450 455

460

Asp Cys Ile Leu Ser Leu Asn Ile Pro Leu His Glu Ala Thr Asn Lys

465 470

475

480

Asp Glu Leu Glu Ala Phe His Lys Gln Lys Ala Gly Lys Gly Leu Glu

485 490

495

Glu Asn Asp Met Arg Ser Ser Asp Glu Ile Val Arg Pro Arg Val Pro

500 505

510

Leu Glu Ala Cys Leu Ala Asn Phe Ala Ser Ser Glu Pro Ile Glu Asp

515 520

525

Tyr Tyr Ser Ser Ala Leu Lys Gly Met Thr Thr Ala Ile Lys Thr Thr

530 535

540

Gly Leu Thr Ser Phe Pro Asp Tyr Leu Val Leu His Met Arg Lys Phe

545 550

555

560

Val Met Glu Glu Gly Trp Val Pro Lys Lys Leu Asp Val Tyr Ile Asp

565 570

575

Val Pro Asp Val Ile Asp Ile Ser His Met Arg Ser Lys Gly Leu Gln

580 585

590

Pro Gly Glu Glu Leu Leu Pro Asp Gly Val Pro Glu Glu Val Met Glu

595 600

605

Ser Ala Gln Pro Val Ala Asn Glu Glu Ile Val Ala Gln Leu Val Ser

610 615

620

Met Gly Phe Ser Gln Leu His Cys Gln Lys Ala Ala Ile Asn Thr Ser

625 630

635

640

Asn Ala Gly Val Glu Glu Ala Met Asn Trp Leu Leu Ser His Met Asp

645 650

655

Asp Pro Asp Ile Asp Ala Pro Ile Ser His Gln Thr Ser Asp Ile Asp

660 665

670

Gln Ser Ser Val Asp Thr Leu Leu Ser Phe Gly Phe Ala Glu Asp Val

675 680

685

Ala Arg Lys Ala Leu Lys Ala Ser Gly Gly Asp Ile Glu Lys Ala Thr
 690 695 700

Asp Trp Val Phe Asn Asn Pro Asn Ala Ser Val Ser Asp Met Asp Val
 705 710 715 720

Ser Ser Ser Asn Ser Ala Gln Thr Pro Ala Gln Ser Gly Leu Pro Asp
 725 730 735

Gly Gly Gly Lys Tyr Lys Leu Phe Gly Ile Val Ser His Met Gly Thr
 740 745 750

Ser Val His Cys Gly His Tyr Val Ala His Ile Leu Lys Glu Gly Arg
 755 760 765

Trp Val Ile Phe Asn Asp Asp Lys Val Gly Ile Ser Thr Asp Pro Pro
 770 775 780

Lys Asp Met Gly Tyr Val Tyr Phe Phe Gln Arg Leu Asp
 785 790 795

<210> 31

<211> 1068

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (1)..(1068)

<223> 15377

<400> 31

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 Met Ile Leu Arg Arg Phe Ile Cys Tyr Asn Ala Ser Ser Thr Val Ser
 1 5 10 15

48

tct ata gct cca tca ccg aag aag cct ctc atc ttc tta ggc tct
 Ser Ile Ala Pro Ser Pro Lys Lys Pro Leu Ile Phe Leu Gly Ser
 20 25 30

96

cct cag gtc tcc gtg agt gtg ctt gaa gct ctt ttc aat gca tct aat
 Pro Gln Val Ser Val Ser Val Leu Glu Ala Leu Phe Asn Ala Ser Asn
 35 40 45

144

gct cca aac tct tcc ttc gag gtt gca ggt att gtt aca cag cct cca	50	55	60	192
Ala Pro Asn Ser Ser Phe Glu Val Ala Gly Ile Val Thr Gln Pro Pro				
tca agg aga gat agg ggt aaa aaa gtg ttg cct tca cca gta gcg caa	65	70	75	240
Ser Arg Arg Asp Arg Gly Lys Lys Val Leu Pro Ser Pro Val Ala Gln				
tac gct ctt gat aaa ggc tta cct tct gat ctc att ttc tcc cct gag	85	90	95	288
Tyr Ala Leu Asp Lys Gly Leu Pro Ser Asp Leu Ile Phe Ser Pro Glu				
aag gca gga gat gaa gca ttt tta tcg gct tta aga gag ttg caa cct	100	105	110	336
Lys Ala Gly Asp Glu Ala Phe Leu Ser Ala Leu Arg Glu Leu Gln Pro				
gag ctt tgt att aca gca gct tat ggg aat att ttg cct act aag ttc	115	120	125	384
Glu Leu Cys Ile Thr Ala Ala Tyr Gly Asn Ile Leu Pro Thr Lys Phe				
ctt aag att ccg gta cat ggg aca gtg aac ata cac cca agt ttg ctg	130	135	140	432
Leu Lys Ile Pro Val His Gly Thr Val Asn Ile His Pro Ser Leu Leu				
ccg ctg tac cgt ggt gca gct cca gtt caa aga gca tta cag gat ggt	145	150	155	480
Pro Leu Tyr Arg Gly Ala Ala Pro Val Gln Arg Ala Leu Gln Asp Gly				
gtc ccg gaa aca gga gta tca tta gca ttt act gtg cgt aag tta gat	165	170	175	528
Val Pro Glu Thr Gly Val Ser Leu Ala Phe Thr Val Arg Lys Leu Asp				
gca ggg cca gtg att gcc tct aag agg ttc caa gtg gat gat cta ata	180	185	190	576
Ala Gly Pro Val Ile Ala Ser Lys Arg Phe Gln Val Asp Asp Leu Ile				
aag gca cca gaa cta ctc tcg ttc cta ttt tct gaa ggt tct aat ctt	195	200	205	624
Lys Ala Pro Glu Leu Leu Ser Phe Leu Phe Ser Glu Gly Ser Asn Leu				
ctt atc cgt gaa ctt ccc tcg ata ttt gat ggg tcc gca aaa tca aaa	210	215	220	672
Leu Ile Arg Glu Leu Pro Ser Ile Phe Asp Gly Ser Ala Lys Ser Lys				
gca gct ccc caa gat gat tct aaa gct acc tta gct cca aag ata gct	225	230	235	720
Ala Ala Pro Gln Asp Asp Ser Lys Ala Thr Leu Ala Pro Lys Ile Ala				
cca gat gag gct tgg ctc tct ttt gac cag gaa gct ttt gtt cta cat	245	250	255	768
Pro Asp Glu Ala Trp Leu Ser Phe Asp Gln Glu Ala Phe Val Leu His				
aac aag gtt cgt gca ttt gca gga tgg ccg gga aca cga gca aaa gtt	260	265	270	816
Asn Lys Val Arg Ala Phe Ala Gly Trp Pro Gly Thr Arg Ala Lys Val				
gta gtc ctt gat gag aaa agc ggt cag caa aat gtg cta gag ctt aaa	275	280	285	864
Val Val Leu Asp Glu Lys Ser Gly Gln Gln Asn Val Leu Glu Leu Lys				

att atg tcc act cga gta tgc aaa gat ctg gaa att cag gat agt gaa 912
 Ile Met Ser Thr Arg Val Cys Lys Asp Leu Glu Ile Gln Asp Ser Glu
 290 295 300

caa gat tat gta act ttc aag aaa ggt tca cta ata ttt ccc tgc aga 960
 Gln Asp Tyr Val Thr Phe Lys Lys Ser Leu Ile Phe Pro Cys Arg
 305 310 315 320

gga ggt aca gct tta gag gta ctg gaa gtc cag ctt cct ggt aag aaa 1008
 Gly Gly Thr Ala Leu Glu Val Leu Glu Val Gln Leu Pro Gly Lys Lys
 325 330 335

gcc atc aac gca gct gct ttt tgg aat ggc ttg aga ggt caa aag ctg 1056
 Ala Ile Asn Ala Ala Ala Phe Trp Asn Gly Leu Arg Gly Gln Lys Leu
 340 345 350

aag aag cta tga 1068
 Lys Lys Leu
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<210> 32

<211> 355

<212> PRT

<213> *Arabidopsis thaliana*

<400> 32

Met Ile Leu Arg Arg Phe Ile Cys Tyr Asn Ala Ser Ser Thr Val Ser 15
 1 5 10 15

Ser Ile Ala Pro Ser Pro Lys Lys Lys Pro Leu Ile Phe Leu Gly Ser
 20 25 30

Pro Gln Val Ser Val Leu Glu Ala Leu Phe Asn Ala Ser Asn
 35 40 45

Ala Pro Asn Ser Ser Phe Glu Val Ala Gly Ile Val Thr Gln Pro Pro
 50 55 60

Ser Arg Arg Asp Arg Gly Lys Lys Val Leu Pro Ser Pro Val Ala Gln
 65 70 75 80

Tyr Ala Leu Asp Lys Gly Leu Pro Ser Asp Leu Ile Phe Ser Pro Glu
 85 90 95

Lys Ala Gly Asp Glu Ala Phe Leu Ser Ala Leu Arg Glu Leu Gln Pro
 100 105 110

Glu Leu Cys Ile Thr Ala Ala Tyr Gly Asn Ile Leu Pro Thr Lys Phe
115 120 125

Leu Lys Ile Pro Val His Gly Thr Val Asn Ile His Pro Ser Leu Leu
130 135 140

Pro Leu Tyr Arg Gly Ala Ala Pro Val Gln Arg Ala Leu Gln Asp Gly
145 150 155 160

Val Pro Glu Thr Gly Val Ser Leu Ala Phe Thr Val Arg Lys Leu Asp
165 170 175

Ala Gly Pro Val Ile Ala Ser Lys Arg Phe Gln Val Asp Asp Leu Ile
180 185 190

Lys Ala Pro Glu Leu Leu Ser Phe Leu Phe Ser Glu Gly Ser Asn Leu
195 200 205

Leu Ile Arg Glu Leu Pro Ser Ile Phe Asp Gly Ser Ala Lys Ser Lys
210 215 220

Ala Ala Pro Gln Asp Asp Ser Lys Ala Thr Leu Ala Pro Lys Ile Ala
225 230 235 240

Pro Asp Glu Ala Trp Leu Ser Phe Asp Gln Glu Ala Phe Val Leu His
245 250 255

Asn Lys Val Arg Ala Phe Ala Gly Trp Pro Gly Thr Arg Ala Lys Val
260 265 270

Val Val Leu Asp Glu Lys Ser Gly Gln Gln Asn Val Leu Glu Leu Lys
275 280 285

Ile Met Ser Thr Arg Val Cys Lys Asp Leu Glu Ile Gln Asp Ser Glu
290 295 300

Gln Asp Tyr Val Thr Phe Lys Lys Gly Ser Leu Ile Phe Pro Cys Arg
305 310 315 320

Gly Gly Thr Ala Leu Glu Val Leu Glu Val Gln Leu Pro Gly Lys Lys
325 330 335

Ala Ile Asn Ala Ala Phe Trp Asn Gly Leu Arg Gly Gln Lys Leu
340 345 350

Lys Lys Leu
355

<210> 33

<211> 2220

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (1)..(2220)

<223> 16219

<400> 33		
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Met Gly Thr Ser Val Gln Val Thr Pro Leu Cys Gly Val Tyr Asn Glu		
1 5 10 15		
aat cct ctc tcc tac tta gtc tcc att gat ggt ttc aac ttc ctc atc		96
Asn Pro Leu Ser Tyr Leu Val Ser Ile Asp Gly Phe Asn Phe Leu Ile		
20 25 30		
gac tgt ggt tgg aac gat ctc ttc gac aca tcg ctc ctc gaa cct ctc		144
Asp Cys Gly Trp Asn Asp Leu Phe Asp Thr Ser Leu Leu Glu Pro Leu		
35 40 45		
ccc agg gtt gct tct act ata gat gca gtt ttg ctt tct cat cca gat		192
Pro Arg Val Ala Ser Thr Ile Asp Ala Val Leu Leu Ser His Pro Asp		
50 55 60		
aca ctt cac att ggt gct ctt cct tat gct atg aag cag ctt gga ctc		240
Thr Leu His Ile Gly Ala Leu Pro Tyr Ala Met Lys Gln Leu Gly Leu		
65 70 75 80		
tcc gct cct gtt tat gct act gag cct gtt cat aga tta ggt ctc ctt		288
Ser Ala Pro Val Tyr Ala Thr Glu Pro Val His Arg Leu Gly Leu Leu		
85 90 95		
aca atg tat gat cag ttt ttg tcc agg aag caa gta tcc gac ttt gat		336
Thr Met Tyr Asp Gln Phe Leu Ser Arg Lys Gln Val Ser Asp Phe Asp		
100 105 110		
ctg ttt aca ctg gat gac ata gat tct gct ttc cag aat gtg atc aga		384
Leu Phe Thr Leu Asp Asp Ile Asp Ser Ala Phe Gln Asn Val Ile Arg		
115 120 125		
ttg act tac tct caa aat tac cat ctt tct gga aag gga gag ggt att		432

Leu Thr Tyr Ser Gln Asn Tyr His Leu Ser Gly Lys Gly Glu Gly Ile			
130	135	140	
gta att gct cct cat gtt gct gga cac atg ctg gga ggt agc atc tgg			480
Val Ile Ala Pro His Val Ala Gly His Met Leu Gly Gly Ser Ile Trp			
145	150	155	160
agg ata aca aag gat ggg gag gat gtt ata tat gct gtt gac tac aat			528
Arg Ile Thr Lys Asp Gly Glu Asp Val Ile Tyr Ala Val Asp Tyr Asn			
165	170	175	
cat cgg aaa gaa agg cat ttg aat gga act gtt tta cag tct ttt gtt			576
His Arg Lys Glu Arg His Leu Asn Gly Thr Val Leu Gln Ser Phe Val			
180	185	190	
cg ^g cct gct gtt ctg ata acc gat gca tat cat gct ctt tat acc aat			624
Arg Pro Ala Val Leu Ile Thr Asp Ala Tyr His Ala Leu Tyr Thr Asn			
195	200	205	
caa acc gca aga cag caa agg gac aaa gaa ttt cta gat acc att tca			672
Gln Thr Ala Arg Gln Gln Arg Asp Lys Glu Phe Leu Asp Thr Ile Ser			
210	215	220	
aaa cat ctt gaa gtt gga gga aat gtt cta ttg cca gta gac act gcg			720
Lys His Leu Glu Val Gly Gly Asn Val Leu Leu Pro Val Asp Thr Ala			
225	230	235	240
ggt cgt gtc ctg gaa ctt ctc ttg ata ctt gaa cag cat tgg tca caa			768
Gly Arg Val Leu Glu Leu Leu Ile Leu Glu Gln His Trp Ser Gln			
245	250	255	
aga ggt ttc agc ttt ccc att tat ttt ctc acg tac gtg tca tct agc			816
Arg Gly Phe Ser Phe Pro Ile Tyr Phe Leu Thr Tyr Val Ser Ser Ser			
260	265	270	
aca att gac tat gtt aag agt ttc ctc gag tgg atg agt gac tcc att			864
Thr Ile Asp Tyr Val Lys Ser Phe Leu Glu Trp Met Ser Asp Ser Ile			
275	280	285	
tca aag tcc ttt gag act tca cgt gat aat gcc ttt cta ttg agg cat			912
Ser Lys Ser Phe Glu Thr Ser Arg Asp Asn Ala Phe Leu Leu Arg His			
290	295	300	
gtc act ctg ttg ata aac aag act gat ctg gat aat gct cca cct ggt			960
Val Thr Leu Leu Ile Asn Lys Thr Asp Leu Asp Asn Ala Pro Pro Gly			
305	310	315	320
cca aag gtt ctt gct tcc atg gct agt ctc gaa gcc ggt ttt gct			1008
Pro Lys Val Val Leu Ala Ser Met Ala Ser Leu Glu Ala Gly Phe Ala			
325	330	335	
cga gag ata ttc gtg gag tgg gca aat gat ccc aga aat tta gtc ctc			1056
Arg Glu Ile Phe Val Glu Trp Ala Asn Asp Pro Arg Asn Leu Val Leu			
340	345	350	
ttt act gaa aca ggc cag ttt ggc act tta gct cgt atg ctt cag tca			1104
Phe Thr Glu Thr Gly Gln Phe Gly Thr Leu Ala Arg Met Leu Gln Ser			
355	360	365	
gcc cca cct cca aaa ttt gtt aaa gtc acc atg tct aag agg gtt cct			1152

Ala Pro Pro Pro Lys Phe Val Lys Val Thr Met Ser Lys Arg Val Pro			
370	375	380	
ttg gct ggg gaa gag tta att gca tat gag gaa gag caa aac aga ctg		1200	
Leu Ala Gly Glu Glu Leu Ile Ala Tyr Glu Glu Gln Asn Arg Leu			
385	390	395	400
aaa agg gaa gaa gct ttg cga gct agc ctc gtt aaa gag gag gaa aca		1248	
Lys Arg Glu Glu Ala Leu Arg Ala Ser Leu Val Lys Glu Glu Thr			
405	410	415	
aaa gct tcc cat gga tcc gat gat aat tca agt gaa cct atg atc ata		1296	
Lys Ala Ser His Gly Ser Asp Asp Asn Ser Ser Glu Pro Met Ile Ile			
420	425	430	
gat acc aag act act cac gat gtt gtt ggt tct cac ggg cct gca tat		1344	
Asp Thr Lys Thr His Asp Val Val Gly Ser His Gly Pro Ala Tyr			
435	440	445	
aaa gat ata ttg att gat gga ttt gtt ccc cca tcg agc agc gta gct		1392	
Lys Asp Ile Leu Ile Asp Gly Phe Val Pro Pro Ser Ser Ser Val Ala			
450	455	460	
cca atg ttc cca tat tat gat aac aca tct gaa tgg gac gac ttt ggg		1440	
Pro Met Phe Pro Tyr Tyr Asp Asn Thr Ser Glu Trp Asp Asp Phe Gly			
465	470	475	480
gag att att aat cca gat gac tat gtg atc aag gat gaa gac atg gac		1488	
Glu Ile Ile Asn Pro Asp Asp Tyr Val Ile Lys Asp Glu Asp Met Asp			
485	490	495	
cga gga gca atg cat aac gga ggt gat gtg gac gga agg ctt gat gag		1536	
Arg Gly Ala Met His Asn Gly Gly Asp Val Asp Gly Arg Leu Asp Glu			
500	505	510	
gca act gct agt ctc atg ctt gat aca aga cct tcg aaa gtc atg tcc		1584	
Ala Thr Ala Ser Leu Met Leu Asp Thr Arg Pro Ser Lys Val Met Ser			
515	520	525	
aat gag ctc att gtg act gtt agt tgt tca ctt gtt aaa atg gac tat		1632	
Asn Glu Leu Ile Val Thr Val Ser Cys Ser Leu Val Lys Met Asp Tyr			
530	535	540	
gaa ggt cgg tca gat ggc cgc tca atc aag tca atg att gcg cat gtt		1680	
Glu Gly Arg Ser Asp Gly Arg Ser Ile Lys Ser Met Ile Ala His Val			
545	550	555	560
tct cct cta aaa ctt gtt ttg gtg cac gcg ata gct gag gct aca gag		1728	
Ser Pro Leu Lys Leu Val Leu Val His Ala Ile Ala Glu Ala Thr Glu			
565	570	575	
cat ttg aag caa cac tgc ttg aac aac atc tgt cca cac gtg tat gct		1776	
His Leu Lys Gln His Cys Leu Asn Asn Ile Cys Pro His Val Tyr Ala			
580	585	590	
cct caa ata gag gaa acg gtc gat gtg act tct gat tta tgt gct tac		1824	
Pro Gln Ile Glu Glu Thr Val Asp Val Thr Ser Asp Leu Cys Ala Tyr			
595	600	605	
aag gtc caa ctt tct gaa aag ctg atg agc aat gtg atc ttc aag aag		1872	

Lys Val Gln Leu Ser Glu Lys Leu Met Ser Asn Val Ile Phe Lys Lys			
610	615	620	
ctg gga gat tca gaa gta gct tgg gtg gat tcc gaa gta ggg aag aca			1920
Leu Gly Asp Ser Glu Val Ala Trp Val Asp Ser Glu Val Gly Lys Thr			
625	630	635	640
gag agg gac atg agg tct cta cta ccg atg cca ggt gct gct tcg cca			1968
Glu Arg Asp Met Arg Ser Leu Leu Pro Met Pro Gly Ala Ala Ser Pro			
645	650	655	
cac aaa cct gtt cta gta ggt gat ctg aaa atc gca gac ttc aag cag			2016
His Lys Pro Val Leu Val Gly Asp Leu Lys Ile Ala Asp Phe Lys Gln			
660	665	670	
ttt ctg tcg agc aag ggt gtt cag gta gaa ttt gca ggt gga gga gct			2064
Phe Leu Ser Ser Lys Gly Val Gln Val Glu Phe Ala Gly Gly Ala			
675	680	685	
tta cgt tgt ggt gaa tat gtc act cta cga aag gtt gga ccg acg ggt			2112
Leu Arg Cys Gly Glu Tyr Val Thr Leu Arg Lys Val Gly Pro Thr Gly			
690	695	700	
caa aag gga gga gca tcg ggt cca cag caa att ctg ata gaa gga ccg			2160
Gln Lys Gly Gly Ala Ser Gly Pro Gln Gln Ile Leu Ile Glu Gly Pro			
705	710	715	720
ttg tgt gaa gac tat tac aaa atc agg gat tat ctc tat tct cag ttc			2208
Leu Cys Glu Asp Tyr Tyr Lys Ile Arg Asp Tyr Leu Tyr Ser Gln Phe			
725	730	735	
tac ctc ctc tga			2220
Tyr Leu Leu			

<210> 34

<211> 739

<212> PRT

<213> *Arabidopsis thaliana*

<400> 34

Met Gly Thr Ser Val Gln Val Thr Pro Leu Cys Gly Val Tyr Asn Glu			
1	5	10	15

Asn Pro Leu Ser Tyr Leu Val Ser Ile Asp Gly Phe Asn Phe Leu Ile			
20	25	30	

Asp Cys Gly Trp Asn Asp Leu Phe Asp Thr Ser Leu Leu Glu Pro Leu			
35	40	45	

Pro Arg Val Ala Ser Thr Ile Asp Ala Val Leu Leu Ser His Pro Asp
50 55 60

Thr Leu His Ile Gly Ala Leu Pro Tyr Ala Met Lys Gln Leu Gly Leu
65 70 75 80

Ser Ala Pro Val Tyr Ala Thr Glu Pro Val His Arg Leu Gly Leu Leu
85 90 95

Thr Met Tyr Asp Gln Phe Leu Ser Arg Lys Gln Val Ser Asp Phe Asp
100 105 110

Leu Phe Thr Leu Asp Asp Ile Asp Ser Ala Phe Gln Asn Val Ile Arg
115 120 125

Leu Thr Tyr Ser Gln Asn Tyr His Leu Ser Gly Lys Gly Glu Gly Ile
130 135 140

Val Ile Ala Pro His Val Ala Gly His Met Leu Gly Gly Ser Ile Trp
145 150 155 160

Arg Ile Thr Lys Asp Gly Glu Asp Val Ile Tyr Ala Val Asp Tyr Asn
165 170 175

His Arg Lys Glu Arg His Leu Asn Gly Thr Val Leu Gln Ser Phe Val
180 185 190

Arg Pro Ala Val Leu Ile Thr Asp Ala Tyr His Ala Leu Tyr Thr Asn
195 200 205

Gln Thr Ala Arg Gln Gln Arg Asp Lys Glu Phe Leu Asp Thr Ile Ser
210 215 220

Lys His Leu Glu Val Gly Gly Asn Val Leu Leu Pro Val Asp Thr Ala
225 230 235 240

Gly Arg Val Leu Glu Leu Leu Ile Leu Glu Gln His Trp Ser Gln
245 250 255

Arg Gly Phe Ser Phe Pro Ile Tyr Phe Leu Thr Tyr Val Ser Ser Ser
260 265 270

Thr Ile Asp Tyr Val Lys Ser Phe Leu Glu Trp Met Ser Asp Ser Ile
275 280 285

Ser Lys Ser Phe Glu Thr Ser Arg Asp Asn Ala Phe Leu Leu Arg His
290 295 300

Val Thr Leu Leu Ile Asn Lys Thr Asp Leu Asp Asn Ala Pro Pro Gly
305 310 315 320

Pro Lys Val Val Leu Ala Ser Met Ala Ser Leu Glu Ala Gly Phe Ala
325 330 335

Arg Glu Ile Phe Val Glu Trp Ala Asn Asp Pro Arg Asn Leu Val Leu
340 345 350

Phe Thr Glu Thr Gly Gln Phe Gly Thr Leu Ala Arg Met Leu Gln Ser
355 360 365

Ala Pro Pro Pro Lys Phe Val Lys Val Thr Met Ser Lys Arg Val Pro
370 375 380

Leu Ala Gly Glu Glu Leu Ile Ala Tyr Glu Glu Glu Gln Asn Arg Leu
385 390 395 400

Lys Arg Glu Glu Ala Leu Arg Ala Ser Leu Val Lys Glu Glu Glu Thr
405 410 415

Lys Ala Ser His Gly Ser Asp Asp Asn Ser Ser Glu Pro Met Ile Ile
420 425 430

Asp Thr Lys Thr Thr His Asp Val Val Gly Ser His Gly Pro Ala Tyr
435 440 445

Lys Asp Ile Leu Ile Asp Gly Phe Val Pro Pro Ser Ser Val Ala
450 455 460

Pro Met Phe Pro Tyr Tyr Asp Asn Thr Ser Glu Trp Asp Asp Phe Gly
465 470 475 480

Glu Ile Ile Asn Pro Asp Asp Tyr Val Ile Lys Asp Glu Asp Met Asp
485 490 495

Arg Gly Ala Met His Asn Gly Gly Asp Val Asp Gly Arg Leu Asp Glu
500 505 510

Ala Thr Ala Ser Leu Met Leu Asp Thr Arg Pro Ser Lys Val Met Ser
515 520 525

Asn Glu Leu Ile Val Thr Val Ser Cys Ser Leu Val Lys Met Asp Tyr
530 535 540

Glu Gly Arg Ser Asp Gly Arg Ser Ile Lys Ser Met Ile Ala His Val
545 550 555 560

Ser Pro Leu Lys Leu Val Leu Val His Ala Ile Ala Glu Ala Thr Glu
565 570 575

His Leu Lys Gln His Cys Leu Asn Asn Ile Cys Pro His Val Tyr Ala
580 585 590

Pro Gln Ile Glu Glu Thr Val Asp Val Thr Ser Asp Leu Cys Ala Tyr
595 600 605

Lys Val Gln Leu Ser Glu Lys Leu Met Ser Asn Val Ile Phe Lys Lys
610 615 620

Leu Gly Asp Ser Glu Val Ala Trp Val Asp Ser Glu Val Gly Lys Thr
625 630 635 640

Glu Arg Asp Met Arg Ser Leu Leu Pro Met Pro Gly Ala Ala Ser Pro
645 650 655

His Lys Pro Val Leu Val Gly Asp Leu Lys Ile Ala Asp Phe Lys Gln
660 665 670

Phe Leu Ser Ser Lys Gly Val Gln Val Glu Phe Ala Gly Gly Ala
675 680 685

Leu Arg Cys Gly Glu Tyr Val Thr Leu Arg Lys Val Gly Pro Thr Gly
690 695 700

Gln Lys Gly Gly Ala Ser Gly Pro Gln Gln Ile Leu Ile Glu Gly Pro
705 710 715 720

Leu Cys Glu Asp Tyr Tyr Lys Ile Arg Asp Tyr Leu Tyr Ser Gln Phe
725 730 735

Tyr Leu Leu

<210> 35

<211> 1116

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (1116)

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att ttg agg ata aca cct gat ttc gct gtt ctt ctc ggg ttg cag cag Ile Leu Arg Ile Thr Pro Asp Phe Ala Val Leu Leu Gly Leu Gln Gln 180 185 190	576
agt ctg tct cct tct aga aac aat gga tta ctt aat atg ctt aag ctg Ser Leu Ser Pro Ser Arg Asn Asn Gly Leu Leu Asn Met Leu Lys Leu 195 200 205	624
atg cag aaa aag gct ctt cat ttg gaa gtc aaa ggt gag gaa gat tca Met Gln Lys Lys Ala Leu His Leu Glu Val Lys Gly Glu Glu Asp Ser 210 215 220	672
agt tct gga gag agt tca gaa tcc agc ttt gtg tct att cct gag act Ser Ser Gly Glu Ser Ser Glu Ser Phe Val Ser Ile Pro Glu Thr 225 230 235 240	720
aag gac gaa gct aat gtt ccg gag gtg gat ttg gag tct aaa cct gat Lys Asp Glu Ala Asn Val Pro Glu Val Asp Leu Glu Ser Lys Pro Asp 245 250 255	768
cta gtt gag gat ttg gga aca gaa aag att gat gat tct gag agt ggg Leu Val Glu Asp Leu Gly Thr Glu Lys Ile Asp Asp Ser Glu Ser Gly 260 265 270	816
tca aat gtt gtt gct tta ggg agt aga ggg atg agg ata aga gag aaa Ser Asn Val Val Ala Leu Gly Ser Arg Gly Met Arg Ile Arg Glu Lys 275 280 285	864
ttg gag aag gag cta gat cct gtt gag tta gaa gtt gaa gat gtt tct Leu Glu Lys Glu Leu Asp Pro Val Glu Leu Glu Val Glu Asp Val Ser 290 295 300	912
tac cag cac gca gga cat gcc gct gtt aga ggt agt gct ggt gat gat Tyr Gln His Ala Gly His Ala Val Arg Gly Ser Ala Gly Asp Asp 305 310 315 320	960
ggg gaa aca cat ttc aac ttg cga atc gtt tcg gat gct ttc caa ggt Gly Glu Thr His Phe Asn Leu Arg Ile Val Ser Asp Ala Phe Gln Gly 325 330 335	1008
aaa agc ttg gtc aag aga cat agg ctg ata tat gac ttg ttg caa gat Lys Ser Leu Val Lys Arg His Arg Leu Ile Tyr Asp Leu Leu Gln Asp 340 345 350	1056
gag ttg aag agc ggg tta cat gct ctc tct att gtg gca aag act cct Glu Leu Lys Ser Gly Leu His Ala Leu Ser Ile Val Ala Lys Thr Pro 355 360 365	1104
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<210> 36

<211> 371

<212> PRT

<213> *Arabidopsis thaliana*

<400> 36

Met Ala Ala Ala Met Ser Ser Ser Cys Cys Ala Ser Ser Leu Arg Leu
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Ile Pro Phe Lys Arg Thr Leu Phe Ser Ser Ile His Tyr Pro Ala Lys
20 25 30

Thr Leu Leu Leu Arg Pro Leu Lys Pro Ser Glu Val Pro Ser Phe Arg
35 40 45

Arg Thr Ile Ile Thr Phe Gln Lys Ile Ser Thr Gly Ile Val Pro Pro
50 55 60

Pro Ser Ala Ser Ser Ser Pro Ser Ser Tyr Gly Asp Leu Gln Pro Ile
65 70 75 80

Glu Glu Leu Pro Pro Lys Leu Gln Glu Ile Val Lys Leu Phe Gln Ser
85 90 95

Val Gln Glu Pro Lys Ala Lys Tyr Glu Gln Leu Met Phe Tyr Gly Lys
100 105 110

Asn Leu Thr Pro Leu Asp Ser Gln Phe Lys Thr Arg Glu Asn Lys Val
115 120 125

Glu Gly Cys Val Ser Gln Val Trp Val Arg Ala Phe Phe Asp Glu Glu
130 135 140

Arg Asn Val Val Tyr Glu Ala Asp Ser Asp Ser Val Leu Thr Lys Gly
145 150 155 160

Leu Ala Ala Leu Leu Val Lys Gly Leu Ser Gly Arg Pro Val Pro Glu
165 170 175

Ile Leu Arg Ile Thr Pro Asp Phe Ala Val Leu Leu Gly Leu Gln Gln
180 185 190

Ser Leu Ser Pro Ser Arg Asn Asn Gly Leu Leu Asn Met Leu Lys Leu
195 200 205

Met Gln Lys Lys Ala Leu His Leu Glu Val Lys Gly Glu Glu Asp Ser
210 215 220

Ser Ser Gly Glu Ser Ser Glu Ser Ser Phe Val Ser Ile Pro Glu Thr
225 230 235 240

Lys Asp Glu Ala Asn Val Pro Glu Val Asp Leu Glu Ser Lys Pro Asp
245 250 255

Leu Val Glu Asp Leu Gly Thr Glu Lys Ile Asp Asp Ser Glu Ser Gly
260 265 270

Ser Asn Val Val Ala Leu Gly Ser Arg Gly Met Arg Ile Arg Glu Lys
275 280 285

Leu Glu Lys Glu Leu Asp Pro Val Glu Leu Glu Val Glu Asp Val Ser
290 295 300

Tyr Gln His Ala Gly His Ala Ala Val Arg Gly Ser Ala Gly Asp Asp
305 310 315 320

Gly Glu Thr His Phe Asn Leu Arg Ile Val Ser Asp Ala Phe Gln Gly
325 330 335

Lys Ser Leu Val Lys Arg His Arg Leu Ile Tyr Asp Leu Leu Gln Asp
340 345 350

Glu Leu Lys Ser Gly Leu His Ala Leu Ser Ile Val Ala Lys Thr Pro
355 360 365

Ala Glu Val
370

<210> 37

<211> 1059

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (1)..(1059)

<223> 20933

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1 5 10 15

gaa ggc cac acc gat cgt gtt tgg agc gta gct tgg aac ccc gtt tct 96
Glu Gly His Thr Asp Arg Val Trp Ser Val Ala Trp Asn Pro Val Ser
20 25 30

tct cac gcc gac ggt gtt tca ccg att ctt gct tct tgc agt ggc gat 144
Ser His Ala Asp Gly Val Ser Pro Ile Leu Ala Ser Cys Ser Gly Asp
35 40 45

aac act gtt cga atc tgg gaa caa agc tct ctc tct cgc tcc tgg act 192
Asn Thr Val Arg Ile Trp Glu Gln Ser Ser Leu Ser Arg Ser Trp Thr
50 55 60

tgc aag aca gtt ttg gaa gag acg cat aca aga act gtg agg tcg tgc 240
Cys Lys Thr Val Leu Glu Thr His Thr Arg Thr Val Arg Ser Cys
65 70 75 80

gct tgg tca ccc tca gga cag tta ttg .gcc act gca agt ttt gat ggt 288
Ala Trp Ser Pro Ser Gly Gln Leu Leu Ala Thr Ala Ser Phe Asp Gly
85 90 95

acc act ggc att tgg aag aat tac ggt tct gag ttt gag tgt att tcc 336
Thr Thr Gly Ile Trp Lys Asn Tyr Gly Ser Glu Phe Glu Cys Ile Ser
100 105 110

act ttg gag gga cat gaa aac gaa gtc aaa agt gta tca tgg aat gca 384
Thr Leu Glu Gly His Glu Asn Glu Val Lys Ser Val Ser Trp Asn Ala
115 120 125

tct ggt tca tgc ctt gca aca tgt agt aga gat aag tct gtt tgg att 432
Ser Gly Ser Cys Leu Ala Thr Cys Ser Arg Asp Lys Ser Val Trp Ile
130 135 140

tgg gaa gtg ctt gaa ggg aat gaa tat gac tgt gct gcg gta tta act 480
Trp Glu Val Leu Glu Gly Asn Glu Tyr Asp Cys Ala Ala Val Leu Thr
145 150 155 160

ggg cat aca caa gat gtg aag atg gtt cag tgg cat ccc acc atg gat 528
Gly His Thr Gln Asp Val Lys Met Val Gln Trp His Pro Thr Met Asp
165 170 175

gtt tta ttt tct tgc agt tat gat aac acc atc aag gtt tgg tgg tct 576
Val Leu Phe Ser Cys Ser Tyr Asp Asn Thr Ile Lys Val Trp Trp Ser
180 185 190

gaa gat gat gat ggt gag tat caa tgt gtc caa acc tta ggt gaa tct 624
Glu Asp Asp Asp Gly Glu Tyr Gln Cys Val Gln Thr Leu Gly Glu Ser
195 200 205

aac aac ggt cac tct tca acg gta tgg tcc atc tca ttt aac gct gca 672
Asn Asn Gly His Ser Ser Thr Val Trp Ser Ile Ser Phe Asn Ala Ala
210 215 220

ggg gac aag atg gtc act tgt agt gat gat cta acc ttg aag ata tgg 720

Gly Asp Lys Met Val Thr Cys Ser Asp Asp	Leu Thr Leu Lys Ile Trp			
225	230	235	240	
ggg aca gat att gcc aag atg cag tct ggt gaa gaa tat gca cct tgg				768
Gly Thr Asp Ile Ala Lys Met Gln Ser Gly	Glu Glu Tyr Ala Pro Trp			
245	250	255		
att cat ctt tgt act ctc tct ggc tat cat gac cgt acc ata tac tca				816
Ile His Leu Cys Thr Leu Ser Gly Tyr His Asp Arg Thr Ile Tyr Ser				
260	265	270		
gct cac tgg tca agg gac gac att att gcc agt gga gca ggc gat aat				864
Ala His Trp Ser Arg Asp Asp Ile Ile Ala Ser Gly Ala Gly Asp Asn				
275	280	285		
gct ata cgg ttg ttt gtg gac agc aaa cat gac tct gtt gat gga cct				912
Ala Ile Arg Leu Phe Val Asp Ser Lys His Asp Ser Val Asp Gly Pro				
290	295	300		
tca tat aat ctt ttg ctg aag aag aat aaa gca cat gaa aat gat gta				960
Ser Tyr Asn Leu Leu Lys Lys Asn Lys Ala His Glu Asn Asp Val				
305	310	315	320	
aac tct gtc caa tgg tca ccc ggt gag ggg aac cgg ttg ctt gcg tcg				1008
Asn Ser Val Gln Trp Ser Pro Gly Glu Gly Asn Arg Leu Leu Ala Ser				
325	330	335		
gct agt gat gat ggg atg gtc aag att tgg cag ctt gca act aaa ccg				1056
Ala Ser Asp Asp Gly Met Val Lys Ile Trp Gln Leu Ala Thr Lys Pro				
340	345	350		
tga			1059	
<210> 38				
<211> 352				
<212> PRT				
<213> <i>Arabidopsis thaliana</i>				
<400> 38				
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1	5	10	15	
Glu Gly His Thr Asp Arg Val Trp Ser Val Ala Trp Asn Pro Val Ser				
20	25	30		
Ser His Ala Asp Gly Val Ser Pro Ile Leu Ala Ser Cys Ser Gly Asp				
35	40	45		
Asn Thr Val Arg Ile Trp Glu Gln Ser Ser Leu Ser Arg Ser Trp Thr				
50	55	60		

Cys Lys Thr Val Leu Glu Glu Thr His Thr Arg Thr Val Arg Ser Cys
65 70 75 80

Ala Trp Ser Pro Ser Gly Gln Leu Leu Ala Thr Ala Ser Phe Asp Gly
85 90 95

Thr Thr Gly Ile Trp Lys Asn Tyr Gly Ser Glu Phe Glu Cys Ile Ser
100 105 110

Thr Leu Glu Gly His Glu Asn Glu Val Lys Ser Val Ser Trp Asn Ala
115 120 125

Ser Gly Ser Cys Leu Ala Thr Cys Ser Arg Asp Lys Ser Val Trp Ile
130 135 140

Trp Glu Val Leu Glu Gly Asn Glu Tyr Asp Cys Ala Ala Val Leu Thr
145 150 155 160

Gly His Thr Gln Asp Val Lys Met Val Gln Trp His Pro Thr Met Asp
165 170 175

Val Leu Phe Ser Cys Ser Tyr Asp Asn Thr Ile Lys Val Trp Trp Ser
180 185 190

Glu Asp Asp Asp Gly Glu Tyr Gln Cys Val Gln Thr Leu Gly Glu Ser
195 200 205

Asn Asn Gly His Ser Ser Thr Val Trp Ser Ile Ser Phe Asn Ala Ala
210 215 220

Gly Asp Lys Met Val Thr Cys Ser Asp Asp Leu Thr Leu Lys Ile Trp
225 230 235 240

Gly Thr Asp Ile Ala Lys Met Gln Ser Gly Glu Glu Tyr Ala Pro Trp
245 250 255

Ile His Leu Cys Thr Leu Ser Gly Tyr His Asp Arg Thr Ile Tyr Ser
260 265 270

Ala His Trp Ser Arg Asp Asp Ile Ile Ala Ser Gly Ala Gly Asp Asn
275 280 285

Ala Ile Arg Leu Phe Val Asp Ser Lys His Asp Ser Val Asp Gly Pro
290 295 300

Ser Tyr Asn Leu Leu Leu Lys Lys Asn Lys Ala His Glu Asn Asp Val
 305 310 315 320

Asn Ser Val Gln Trp Ser Pro Gly Glu Gly Asn Arg Leu Leu Ala Ser
 325 330 335

Ala Ser Asp Asp Gly Met Val Lys Ile Trp Gln Leu Ala Thr Lys Pro
 340 345 350

<210> 39

<211> 942

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (1)...(924)

<223>

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1 5 10 15		
gaa tca tca act aag ctc ttc acc aaa aag cct aac aat gtt gtg gtt		96
Glu Ser Ser Thr Lys Leu Phe Thr Lys Lys Pro Asn Asn Val Val Val		
20 25 30		
tgt gcg gcg aga ggt cca aga cct cgg tct cct cgt gta tgg aaa aca		144
Cys Ala Ala Arg Gly Pro Arg Pro Arg Ser Pro Arg Val Trp Lys Thr		
35 40 45		
agg aag agg att gga act atc tct aaa gct gcc aaa atg att gct tgt		192
Arg Lys Arg Ile Gly Thr Ile Ser Lys Ala Ala Lys Met Ile Ala Cys		
50 55 60		
ata aaa gga ttg tcg aat gtt aaa gaa gaa gtt tat gga gcg ctt gat		240
Ile Lys Gly Leu Ser Asn Val Lys Glu Glu Val Tyr Gly Ala Leu Asp		
65 70 75 80		
tcc ttc att gct tgg gaa tta gag ttc cct ctt gtt ata gtt aag aag		288
Ser Phe Ile Ala Trp Glu Leu Glu Phe Pro Leu Val Ile Val Lys Lys		
85 90 95		
gca tta gtt ata ctt gaa gat gaa aaa gaa tgg aag aag att att cag		336
Ala Leu Val Ile Leu Glu Asp Glu Lys Glu Trp Lys Lys Ile Ile Gln		

100	105	110	
gtg aca aaa tgg atg ctg agt aaa ggc caa gga aga aca atg gga act			384
Val Thr Lys Trp Met Leu Ser Lys Gly Gln Gly Arg Thr Met Gly Thr			
115	120	125	
tac ttc tca tta cta aat gct tta gca gaa gat aat cgc ctt gac gaa			432
Tyr. Phe Ser Leu Leu Asn Ala Leu Ala Glu Asp Asn Arg Leu Asp Glu			
130	135	140	
gct gag gaa ttg tgg aac aaa ttg ttc atg gaa cat tta gaa gga act			480
Ala Glu Glu Leu Trp Asn Lys Leu Phe Met Glu His Leu Glu Gly Thr			
145	150	155	160
cct aga aag ttc ttc aac aaa atg atc tct ata tat tac aag aga gat			528
Pro Arg Lys Phe Phe Asn Lys Met Ile Ser Ile Tyr Tyr Lys Arg Asp			
165	170	175	
atg cac caa aag ctc ttc gag gtc ttt gct gac atg gag gag ctt gga			576
Met His Gln Lys Leu Phe Glu Val Phe Ala Asp Met Glu Glu Leu Gly			
180	185	190	
gtg aaa ccg aat gtt gcg att gtg tct atg gtt gga aaa gtg ttt gtg			624
Val Lys Pro Asn Val Ala Ile Val Ser Met Val Gly Lys Val Phe Val			
195	200	205	
aaa cta gag atg aag gat aag tac gag aaa ctg atg aag aaa tat cct			672
Lys Leu Glu Met Lys Asp Lys Tyr Glu Lys Leu Met Lys Lys Tyr Pro			
210	215	220	
cca cca cag tgg gag ttt aga tac atc aaa gga aga cgt gtt aag gtc			720
Pro Pro Gln Trp Glu Phe Arg Tyr Ile Lys Gly Arg Arg Val Lys Val			
225	230	235	240
aag gca aag cag ctg aat gag cta agc gaa ggt gaa ggt ggt tta agc			768
Lys Ala Lys Gln Leu Asn Glu Leu Ser Glu Gly Glu Gly Gly Leu Ser			
245	250	255	
agc gac gaa gat aag att gac aat gag att gag agt gaa gaa gaa gat			816
Ser Asp Glu Asp Lys Ile Asp Asn Glu Ile Glu Ser Glu Glu Glu Asp			
260	265	270	
ggt gag gat ctc agt gaa gag gaa gat gaa aaa gaa ctt ttg ggt			864
Gly Glu Asp Leu Ser Glu Glu Glu Asp Glu Lys Glu Leu Leu Gly			
275	280	285	
gga agt caa gga cag att act tct aga gaa ccc agt ctt gat cat ttg			912
Gly Ser Gln Gly Gln Ile Thr Ser Arg Glu Pro Ser Leu Asp His Leu			
290	295	300	
gac tct tca tga			924
Asp Ser Ser			
305			

<210> 40

<211> 307

<212> PRT

<213> Arabidopsis thaliana

<400> 40

Met Leu Ser Leu Arg Tyr Ser Leu Pro Tyr Leu Leu Leu Gln Thr Arg
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Glu Ser Ser Thr Lys Leu Phe Thr Lys Lys Pro Asn Asn Val Val Val
20 25 30

Cys Ala Ala Arg Gly Pro Arg Pro Arg Ser Pro Arg Val Trp Lys Thr
35 40 45

Arg Lys Arg Ile Gly Thr Ile Ser Lys Ala Ala Lys Met Ile Ala Cys
50 55 60

Ile Lys Gly Leu Ser Asn Val Lys Glu Glu Val Tyr Gly Ala Leu Asp
65 70 75 80

Ser Phe Ile Ala Trp Glu Leu Glu Phe Pro Leu Val Ile Val Lys Lys
85 90 95

Ala Leu Val Ile Leu Glu Asp Glu Lys Glu Trp Lys Lys Ile Ile Gln
100 105 110

Val Thr Lys Trp Met Leu Ser Lys Gly Gln Gly Arg Thr Met Gly Thr
115 120 125

Tyr Phe Ser Leu Leu Asn Ala Leu Ala Glu Asp Asn Arg Leu Asp Glu
130 135 140

Ala Glu Glu Leu Trp Asn Lys Leu Phe Met Glu His Leu Glu Gly Thr
145 150 155 160

Pro Arg Lys Phe Phe Asn Lys Met Ile Ser Ile Tyr Tyr Lys Arg Asp
165 170 175

Met His Gln Lys Leu Phe Glu Val Phe Ala Asp Met Glu Glu Leu Gly
180 185 190

Val Lys Pro Asn Val Ala Ile Val Ser Met Val Gly Lys Val Phe Val
195 200 205

Lys Leu Glu Met Lys Asp Lys Tyr Glu Lys Leu Met Lys Lys Tyr Pro
 210 215 220

Pro Pro Gln Trp Glu Phe Arg Tyr Ile Lys Gly Arg Arg Val Lys Val
 225 230 235 240

Lys Ala Lys Gln Leu Asn Glu Leu Ser Glu Gly Glu Gly Leu Ser
 245 250 255

Ser Asp Glu Asp Lys Ile Asp Asn Glu Ile Glu Ser Glu Glu Asp
 260 265 270

Gly Glu Asp Leu Ser Glu Glu Glu Asp Glu Lys Glu Leu Leu Gly
 275 280 285

Gly Ser Gln Gly Gln Ile Thr Ser Arg Glu Pro Ser Leu Asp His Leu
 290 295 300

Asp Ser Ser
 305

<210> 41

<211> 2427

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (1)..(2427)

<223> 21878

<400> 41
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gga aca tct tct tct tcg tct ctt tca atg acg tta tcc tca aca aac 96
 Gly Thr Ser Ser Ser Ser Leu Ser Met Thr Leu Ser Ser Thr Asn
 20 25 30

gcg tta tcg ttt ttg tcg aaa gga tgg aga gag gta tgg gat tca gca 144
 Ala Leu Ser Phe Leu Ser Lys Gly Trp Arg Glu Val Trp Asp Ser Ala

35	40	45	
gat gcg gat ttg cag ctg atg cga gac aga gct aac tct gtt aag aat Asp Ala Asp Leu Gln Leu Met Arg Asp Arg Ala Asn Ser Val Lys Asn 50	55	60	192
cta gca tca acg ttc gat aga gag atc gag aat ttc ctc aat aac tcg Leu Ala Ser Thr Phe Asp Arg Glu Ile Glu Asn Phe Leu Asn Asn Ser 65	70	75	240
gcg agg tct gcg ttt ccc gtt ggt tca cca tcg gcg tcg tct ttc tca Ala Arg Ser Ala Phe Pro Val Gly Ser Pro Ser Ala Ser Ser Phe Ser 85	90	95	288
aat gaa att ggt atc atg aag ctt cag ccg aag att tcg gag ttt Asn Glu Ile Gly Ile Met Lys Lys Leu Gln Pro Lys Ile Ser Glu Phe 100	105	110	336
cgt agg gtt tat tcg gcg ccg gag att agt cgc aag gtt atg gag aga Arg Arg Val Tyr Ser Ala Pro Glu Ile Ser Arg Lys Val Met Glu Arg 115	120	125	384
tgg gga cct gcg aga gcg aag ctt gga atg gat cta tcg gcg att aag Trp Gly Pro Ala Arg Ala Lys Leu Gly Met Asp Leu Ser Ala Ile Lys 130	135	140	432
aag gcg att gtg tct gag atg gaa ttg gat gag cgt cag gga gtt ttg Lys Ala Ile Val Ser Glu Met Glu Leu Asp Glu Arg Gln Gly Val Leu 145	150	155	480
gag atg agt aga ttg agg aga cgg cgt aat agt gat agg gtt agg ttt Glu Met Ser Arg Leu Arg Arg Arg Asn Ser Asp Arg Val Arg Phe 165	170	175	528
acg gag ttt ttc gcg gag gct gag aga gat gga gaa gct tat ttc ggt Thr Glu Phe Ala Glu Ala Glu Arg Asp Gly Glu Ala Tyr Phe Gly 180	185	190	576
gat tgg gaa ccg att agg tct ttg aag agt aga ttt aaa gag ttt gag Asp Trp Glu Pro Ile Arg Ser Leu Lys Ser Arg Phe Lys Glu Phe Glu 195	200	205	624
aaa cga agc tcg tta gaa ata ttg agt gga ttc aag aac agt gaa ttt Lys Arg Ser Ser Leu Glu Ile Leu Ser Gly Phe Lys Asn Ser Glu Phe 210	215	220	672
gtt gag aag ctc aaa acc agc ttt aaa tca att tac aaa gaa act gat Val Glu Lys Leu Lys Thr Ser Phe Lys Ser Ile Tyr Lys Glu Thr Asp 225	230	235	720
gag gct aag gat gtc cct ccg ttg gat gta cct gaa ctg ttg gca tgt Glu Ala Lys Asp Val Pro Pro Leu Asp Val Pro Glu Leu Leu Ala Cys 245	250	255	768
ttg gtt aga caa tct gaa cct ttt ctt gat cag att ggt gtt aga aag Leu Val Arg Gln Ser Glu Pro Phe Leu Asp Gln Ile Gly Val Arg Lys 260	265	270	816
gat aca tgt gac cga ata gta gaa agc ctt tgc aaa tgc aag agc caa Asp Thr Cys Asp Arg Ile Val Glu Ser Leu Cys Lys Cys Lys Ser Gln			864

275	280	285	
caa ctt tgg cgt ctg cca tct gca caa gca tcc gat tta att gaa aat Gln Leu Trp Arg Leu Pro Ser Ala Gln Ala Ser Asp Leu Ile Glu Asn 290	295	300	912
gat aac cat gga gtt gat ttg gat atg agg ata gcc agt gtt ctt caa Asp Asn His Gly Val Asp Leu Asp Met Arg Ile Ala Ser Val Leu Gln 305	310	315	960
agc aca gga cac cat tat gat ggt ggg ttt tgg act gat ttt gtg aag Ser Thr Gly His His Tyr Asp Gly Gly Trp Thr Asp Phe Val Lys 325	330	335	1008
cct gag aca ccg gaa aac aaa agg cat gtg gca att gtt aca aca gct Pro Glu Thr Pro Glu Asn Lys Arg His Val Ala Ile Val Thr Thr Ala 340	345	350	1056
agt ctt cct tgg atg acc gga aca gct gta aat ccg cta ttc aga gcg Ser Leu Pro Trp Met Thr Gly Thr Ala Val Asn Pro Leu Phe Arg Ala 355	360	365	1104
gcg tat ttg gca aaa gct gca aaa cag agt gtt act ctc gtg gtt cct Ala Tyr Leu Ala Lys Ala Ala Lys Gln Ser Val Thr Leu Val Val Pro 370	375	380	1152
tgg ctc tgc gaa tct gat caa gaa cta gtg tat cca aac aat ctc acc Trp Leu Cys Glu Ser Asp Gln Glu Leu Val Tyr Pro Asn Asn Leu Thr 385	390	395	1200
ttc agc tca cct gaa gaa caa gag agt tat ata cgt aaa tgg ttg gag Phe Ser Ser Pro Glu Glu Gln Glu Ser Tyr Ile Arg Lys Trp Leu Glu 405	410	415	1248
gaa agg att ggt ttc aag gct gat ttt aaa atc tcc ttt tac cca gga Glu Arg Ile Gly Phe Lys Ala Asp Phe Lys Ile Ser Phe Tyr Pro Gly 420	425	430	1296
aag ttt tca aaa gaa agg cgc agc ata ttt cct gct ggt gac act tct Lys Phe Ser Lys Glu Arg Arg Ser Ile Phe Pro Ala Gly Asp Thr Ser 435	440	445	1344
caa ttt ata tcg tca aaa gat gct gac att gct ata ctt gaa gaa cct Gln Phe Ile Ser Ser Lys Asp Ala Asp Ile Ala Ile Leu Glu Glu Pro 450	455	460	1392
gaa cat ctc aac tgg tat tat cac ggc aag cgt tgg act gat aaa ttc Glu His Leu Asn Trp Tyr Tyr His Gly Lys Arg Trp Thr Asp Lys Phe 465	470	475	1440
aac cat gtt gtt gga att gtc cac aca aac tac tta gag tac atc aag Asn His Val Val Gly Ile Val His Thr Asn Tyr Leu Glu Tyr Ile Lys 485	490	495	1488
agg gag aag aat gga gct ctt caa gca ttt ttt gtg aac cat gta aac Arg Glu Lys Asn Gly Ala Leu Gln Ala Phe Phe Val Asn His Val Asn 500	505	510	1536
aat tgg gtc aca cga gcg tat tgt gac aag gtt ctt cgc ctc tct gcg Asn Trp Val Thr Arg Ala Tyr Cys Asp Lys Val Leu Arg Leu Ser Ala			1584

515	520	525	
gca aca caa gat tta cca aag tct gtt gta tgc aat gtc cat ggt gtc Ala Thr Gln Asp Leu Pro Lys Ser Val Val Cys Asn Val His Gly Val			1632
530	535	540	
aat ccc aag ttc ctt atg att ggg gag aaa att gct gaa gag aga tcc Asn Pro Lys Phe Leu Met Ile Gly Glu Lys Ile Ala Glu Glu Arg Ser			1680
545	550	555	560
cgt ggt gaa caa gct ttc tca aaa ggt gca tac ttc tta gga aaa atg Arg Gly Glu Gln Ala Phe Ser Lys Gly Ala Tyr Phe Leu Gly Lys Met			1728
565	570	575	
gtg tgg gct aaa gga tac aga gaa cta ata gat ctg atg gct aaa cac Val Trp Ala Lys Gly Tyr Arg Glu Leu Ile Asp Leu Met Ala Lys His			1776
580	585	590	
aaa agc gaa ctt ggg agc ttc aat cta gat gta tat ggg aac ggt gaa Lys Ser Glu Leu Gly Ser Phe Asn Leu Asp Val Tyr Gly Asn Gly Glu			1824
595	600	605	
gat gca gtc gag gtc caa cgt gca gca aag aaa cat gac ttg aat ctc Asp Ala Val Glu Val Gln Arg Ala Ala Lys Lys His Asp Leu Asn Leu			1872
610	615	620	
aat ttc ctc aaa gga agg gac cac gct gac gat gct ctt cac aag tac Asn Phe Leu Lys Gly Arg Asp His Ala Asp Asp Ala Leu His Lys Tyr			1920
625	630	635	640
aaa gtg ttc ata aac ccc agc atc agc gat gtt cta tgc aca gca acc Lys Val Phe Ile Asn Pro Ser Ile Ser Asp Val Leu Cys Thr Ala Thr			1968
645	650	655	
gca gaa gca cta gcc atg ggg aag ttt gtg gtg tgt gca gat cac cct Ala Glu Ala Leu Ala Met Gly Lys Phe Val Val Cys Ala Asp His Pro			2016
660	665	670	
tca aac gaa ttc ttt aga tca ttc ccg aac tgc tta act tac aaa aca Ser Asn Glu Phe Phe Arg Ser Phe Pro Asn Cys Leu Thr Tyr Lys Thr			2064
675	680	685	
tcc gaa gac ttt gtg tcc aaa gtg caa gaa gca atg acg aaa gag cca Ser Glu Asp Phe Val Ser Lys Val Gln Glu Ala Met Thr Lys Glu Pro			2112
690	695	700	
cta cct ctc act cct gaa caa atg tac aat ctc tct tgg gaa gca gca Leu Pro Leu Thr Pro Glu Gln Met Tyr Asn Leu Ser Trp Glu Ala Ala			2160
705	710	715	720
aca cag agg ttc atg gag tat tca gat ctc gat aag atc tta aac aat Thr Gln Arg Phe Met Glu Tyr Ser Asp Leu Asp Lys Ile Leu Asn Asn			2208
725	730	735	
gga gag gga gga agg aag atg cga aaa tca aga tcg gtt ccg agc ttt Gly Glu Gly Gly Arg Lys Met Arg Lys Ser Arg Ser Val Pro Ser Phe			2256
740	745	750	
aac gag gtg gtc gat gga gga ttg gca ttc tca cac tat gtt cta aca Asn Glu Val Val Asp Gly Gly Leu Ala Phe Ser His Tyr Val Leu Thr			2304

755

760

765

ggg aac gat ttc ttg aga cta tgc act gga gca aca cca aga aca aca aaa 2352
 Gly Asn Asp Phe Leu Arg Leu Cys Thr Gly Ala Thr Pro Arg Thr Lys
 770 775 780

gac tat gat aat caa cat tgc aag gat ctg aat ctc gta cca cct cac 2400
 Asp Tyr Asp Asn Gln His Cys Lys Asp Leu Asn Leu Val Pro Pro His
 785 790 795 800

gtt cac aag cca atc ttc ggc tgg tag 2427
 Val His Lys Pro Ile Phe Gly Trp
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<211> 808

<212> PRT

<213> *Arabidopsis thaliana*

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Ala Leu Ser Phe Leu Ser Lys Gly Trp Arg Glu Val Trp Asp Ser Ala 45
 35 40 45

Asp Ala Asp Leu Gln Leu Met Arg Asp Arg Ala Asn Ser Val Lys Asn 60
 50 55 60

Leu Ala Ser Thr Phe Asp Arg Glu Ile Glu Asn Phe Leu Asn Asn Ser 80
 65 70 75 80

Ala Arg Ser Ala Phe Pro Val Gly Ser Pro Ser Ala Ser Ser Phe Ser 95
 85 90 95

Asn Glu Ile Gly Ile Met Lys Lys Leu Gln Pro Lys Ile Ser Glu Phe 110
 100 105 110

Arg Arg Val Tyr Ser Ala Pro Glu Ile Ser Arg Lys Val Met Glu Arg 125
 115 120 125

Trp Gly Pro Ala Arg Ala Lys Leu Gly Met Asp Leu Ser Ala Ile Lys

130	135	140
Lys Ala Ile Val Ser Glu Met Glu Leu Asp Glu Arg Gln Gly Val Leu		
145	150	155
160		
Glu Met Ser Arg Leu Arg Arg Arg Asn Ser Asp Arg Val Arg Phe		
165	170	175
Thr Glu Phe Phe Ala Glu Ala Glu Arg Asp Gly Glu Ala Tyr Phe Gly		
180	185	190
Asp Trp Glu Pro Ile Arg Ser Leu Lys Ser Arg Phe Lys Glu Phe Glu		
195	200	205
Lys Arg Ser Ser Leu Glu Ile Leu Ser Gly Phe Lys Asn Ser Glu Phe		
210	215	220
Val Glu Lys Leu Lys Thr Ser Phe Lys Ser Ile Tyr Lys Glu Thr Asp		
225	230	235
240		
Glu Ala Lys Asp Val Pro Pro Leu Asp Val Pro Glu Leu Leu Ala Cys		
245	250	255
Leu Val Arg Gln Ser Glu Pro Phe Leu Asp Gln Ile Gly Val Arg Lys		
260	265	270
Asp Thr Cys Asp Arg Ile Val Glu Ser Leu Cys Lys Cys Lys Ser Gln		
275	280	285
Gln Leu Trp Arg Leu Pro Ser Ala Gln Ala Ser Asp Leu Ile Glu Asn		
290	295	300
Asp Asn His Gly Val Asp Leu Asp Met Arg Ile Ala Ser Val Leu Gln		
305	310	315
320		
Ser Thr Gly His His Tyr Asp Gly Gly Phe Trp Thr Asp Phe Val Lys		
325	330	335
Pro Glu Thr Pro Glu Asn Lys Arg His Val Ala Ile Val Thr Thr Ala		
340	345	350
Ser Leu Pro Trp Met Thr Gly Thr Ala Val Asn Pro Leu Phe Arg Ala		
355	360	365
Ala Tyr Leu Ala Lys Ala Ala Lys Gln Ser Val Thr Leu Val Val Pro		

370

375

380

Trp Leu Cys Glu Ser Asp Gln Glu Leu Val Tyr Pro Asn Asn Leu Thr
385 390 395 400

Phe Ser Ser Pro Glu Glu Gln Glu Ser Tyr Ile Arg Lys Trp Leu Glu
405 410 415

Glu Arg Ile Gly Phe Lys Ala Asp Phe Lys Ile Ser Phe Tyr Pro Gly
420 425 430

Lys Phe Ser Lys Glu Arg Arg Ser Ile Phe Pro Ala Gly Asp Thr Ser
435 440 445

Gln Phe Ile Ser Ser Lys Asp Ala Asp Ile Ala Ile Leu Glu Pro
450 455 460

Glu His Leu Asn Trp Tyr Tyr His Gly Lys Arg Trp Thr Asp Lys Phe
465 470 475 480

Asn His Val Val Gly Ile Val His Thr Asn Tyr Leu Glu Tyr Ile Lys
485 490 495

Arg Glu Lys Asn Gly Ala Leu Gln Ala Phe Phe Val Asn His Val Asn
500 505 510

Asn Trp Val Thr Arg Ala Tyr Cys Asp Lys Val Leu Arg Leu Ser Ala
515 520 525

Ala Thr Gln Asp Leu Pro Lys Ser Val Val Cys Asn Val His Gly Val
530 535 540

Asn Pro Lys Phe Leu Met Ile Gly Glu Lys Ile Ala Glu Glu Arg Ser
545 550 555 560

Arg Gly Glu Gln Ala Phe Ser Lys Gly Ala Tyr Phe Leu Gly Lys Met
565 570 575

Val Trp Ala Lys Gly Tyr Arg Glu Leu Ile Asp Leu Met Ala Lys His
580 585 590

Lys Ser Glu Leu Gly Ser Phe Asn Leu Asp Val Tyr Gly Asn Gly Glu
595 600 605

Asp Ala Val Glu Val Gln Arg Ala Ala Lys Lys His Asp Leu Asn Leu

610	615	620
Asn Phe Leu Lys Gly Arg Asp His Ala Asp Asp Ala Leu His Lys Tyr		
625	630	640
Lys Val Phe Ile Asn Pro Ser Ile Ser Asp Val Leu Cys Thr Ala Thr		
645	650	655
Ala Glu Ala Leu Ala Met Gly Lys Phe Val Val Cys Ala Asp His Pro		
660	665	670
Ser Asn Glu Phe Phe Arg Ser Phe Pro Asn Cys Leu Thr Tyr Lys Thr		
675	680	685
Ser Glu Asp Phe Val Ser Lys Val Gln Glu Ala Met Thr Lys Glu Pro		
690	695	700
Leu Pro Leu Thr Pro Glu Gln Met Tyr Asn Leu Ser Trp Glu Ala Ala		
705	710	720
Thr Gln Arg Phe Met Glu Tyr Ser Asp Leu Asp Lys Ile Leu Asn Asn		
725	730	735
Gly Glu Gly Arg Lys Met Arg Lys Ser Arg Ser Val Pro Ser Phe		
740	745	750
Asn Glu Val Val Asp Gly Gly Leu Ala Phe Ser His Tyr Val Leu Thr		
755	760	765
Gly Asn Asp Phe Leu Arg Leu Cys Thr Gly Ala Thr Pro Arg Thr Lys		
770	775	780
Asp Tyr Asp Asn Gln His Cys Lys Asp Leu Asn Leu Val Pro Pro His		
785	790	800
Val His Lys Pro Ile Phe Gly Trp		
805		
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tcc tac atc gct act tct ctc cac gat ctc aac tcc gtc gat ggt ccg	96
Ser Tyr Ile Ala Thr Ser Leu His Asp Leu Asn Ser Val Asp Gly Pro	
20 25 30	
ccg aga gat atc gac ggt atc gga ggc gcc gtt ggt cgt gac ggc gat	144
Pro Arg Asp Ile Asp Gly Ile Gly Ala Val Gly Arg Asp Gly Asp	
35 40 45	
agt tta gat aat gac ggc gat tcc tct tct gcg gac tgt atg cat gaa	192
Ser Leu Asp Asn Asp Gly Asp Ser Ser Ala Asp Cys Met His Glu	
50 55 60	
tca tac aga aac tct atg caa atc gga gta gaa gaa ggt gga tct aac	240
Ser Tyr Arg Asn Ser Met Gln Ile Gly Val Glu Glu Gly Ser Asn	
65 70 75 80	
atg gag aac aaa gga tct gct tac att atg tta aac att gaa gat gtt	288
Met Glu Asn Lys Gly Ser Ala Tyr Ile Met Leu Asn Ile Glu Asp Val	
85 90 95	
tca ccg att gaa gca gca aga ggg agg ttt ctg caa atc ata ttg gac	336
Ser Pro Ile Glu Ala Ala Arg Gly Arg Phe Leu Gln Ile Ile Leu Asp	
100 105 110	
tac ttt att agc caa cat gtg att gaa gtc tgt gag agc aaa cgt gat	384
Tyr Phe Ile Ser Gln His Val Ile Glu Val Cys Glu Ser Lys Arg Asp	
115 120 125	
cat gat gtg gat tca gga gga cgt gat agt aat agt aaa gtg aag agg	432
His Asp Val Asp Ser Gly Gly Arg Asp Ser Asn Ser Lys Val Lys Arg	
130 135 140	
aag tcg gat gat acg cga tat gaa ggt gat ccg agt ttt gcg tta ccg	480
Lys Ser Asp Asp Thr Arg Tyr Glu Gly Asp Pro Ser Phe Ala Leu Pro	
145 150 155 160	
ttg atg tat att gca aat ttg tat gag act tta gtt ggt gaa gca aat	528
Leu Met Tyr Ile Ala Asn Leu Tyr Glu Thr Leu Val Gly Glu Ala Asn	
165 170 175	
gtg agg ctt gct tca ttg aat gga ata agg gat aag act att gga gta	576
Val Arg Leu Ala Ser Leu Asn Gly Ile Arg Asp Lys Thr Ile Gly Val	
180 185 190	

gct ctt gaa gct gct ggt ggc ttg tat agg aaa tta act aag aag ttt Ala Leu Glu Ala Ala Gly Gly Leu Tyr Arg Lys Leu Thr Lys Lys Phe 195 200 205	624
cct aag aaa ggt act tgc atg tac agg aga aga gaa ctg gca act tca Pro Lys Lys Gly Thr Cys Met Tyr Arg Arg Arg Glu Leu Ala Thr Ser 210 215 220	672
gtt gaa aca agg aca aga ttt cca gaa ttg gta ata cat gaa gag aaa Val Glu Thr Arg Thr Arg Phe Pro Glu Leu Val Ile His Glu Glu Lys 225 230 235 240	720
cga gtt cgc ttt gtg gtg gtt aat ggt ttg gat att gtt gaa aag cca Arg Val Arg Phe Val Val Val Asn Gly Leu Asp Ile Val Glu Lys Pro 245 250 255	768
agt gat ttg cct att gaa gaa gct gaa tgg ttt aag cga tta aca ggc Ser Asp Leu Pro Ile Glu Ala Glu Trp Phe Lys Arg Leu Thr Gly 260 265 270	816
cgt aat gaa gtg gct atc tct gct aga gat tat aaa ttc tac tgc cct Arg Asn Glu Val Ala Ile Ser Ala Arg Asp Tyr Lys Phe Tyr Cys Pro 275 280 285	864
cga cgc aag cat agg cgt ctt cag aat tct gtc tcc agc atc aat ggc Arg Arg Lys His Arg Arg Leu Gln Asn Ser Val Ser Ser Ile Asn Gly 290 295 300	912
ttg cct aca ttt cca ggt ata gac tct tca acg tta gct aat aca caa Leu Pro Thr Phe Pro Gly Ile Asp Ser Ser Thr Leu Ala Asn Thr Gln 305 310 315 320	960
gga ttt cgc gaa gat caa agc caa caa cac act cct tct cct tcc Gly Phe Arg Glu Asp Gln Ser Gln Gln His Thr Pro Ser Pro Ser 325 330 335	1008
aaa cat cat atg tca tct ttg tct cat caa ttt cat caa tct att cac Lys His His Met Ser Ser Leu Ser His Gln Phe His Gln Ser Ile His 340 345 350	1056
cag agc cac caa cac cat caa tct ata tac caa agt caa cac gca gcc Gln Ser His Gln His His Gln Ser Ile Tyr Gln Ser Gln His Ala Ala 355 360 365	1104
aca cac tat ccc agt cag aac cat caa tgt gac cct gaa cta tct cac Thr His Tyr Pro Ser Gln Asn His Gln Cys Asp Pro Glu Leu Ser His 370 375 380	1152
aca caa atg gct tgc ttg caa ccc ctc act gga ggc cat gta atg cca Thr Gln Met Ala Cys Leu Gln Pro Leu Thr Gly Gly His Val Met Pro 385 390 395 400	1200
aat agt ccg gcg aaa ttt tgt gac caa tgt gga gca cag tac ttg aga Asn Ser Pro Ala Lys Phe Cys Asp Gln Cys Gly Ala Gln Tyr Leu Arg 405 410 415	1248
gag aca tcc aaa ttc tgc tca gag tgt ggt tcc aag aga ctc ggg ata Glu Thr Ser Lys Phe Cys Ser Glu Cys Gly Ser Lys Arg Leu Gly Ile 420 425 430	1296

tag

1299

<210> 44

<211> 432

<212> PRT

<213> *Arabidopsis thaliana*

<400> 44

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Ser Tyr Ile Ala Thr Ser Leu His Asp Leu Asn Ser Val Asp Gly Pro
20 25 30

Pro Arg Asp Ile Asp Gly Ile Gly Gly Ala Val Gly Arg Asp Gly Asp
35 40 45

Ser Leu Asp Asn Asp Gly Asp Ser Ser Ser Ala Asp Cys Met His Glu
50 55 60

Ser Tyr Arg Asn Ser Met Gln Ile Gly Val Glu Glu Gly Ser Asn
65 70 75 80

Met Glu Asn Lys Gly Ser Ala Tyr Ile Met Leu Asn Ile Glu Asp Val
85 90 95

Ser Pro Ile Glu Ala Ala Arg Gly Arg Phe Leu Gln Ile Ile Leu Asp
100 105 110

Tyr Phe Ile Ser Gln His Val Ile Glu Val Cys Glu Ser Lys Arg Asp
115 120 125

His Asp Val Asp Ser Gly Gly Arg Asp Ser Asn Ser Lys Val Lys Arg
130 135 140

Lys Ser Asp Asp Thr Arg Tyr Glu Gly Asp Pro Ser Phe Ala Leu Pro
145 150 155 160

Leu Met Tyr Ile Ala Asn Leu Tyr Glu Thr Leu Val Gly Glu Ala Asn
165 170 175

Val Arg Leu Ala Ser Leu Asn Gly Ile Arg Asp Lys Thr Ile Gly Val
180 185 190

Ala Leu Glu Ala Ala Gly Gly Leu Tyr Arg Lys Leu Thr Lys Lys Phe
195 200 205

Pro Lys Lys Gly Thr Cys Met Tyr Arg Arg Arg Glu Leu Ala Thr Ser
210 215 220

Val Glu Thr Arg Thr Arg Phe Pro Glu Leu Val Ile His Glu Glu Lys
225 230 235 240

Arg Val Arg Phe Val Val Asn Gly Leu Asp Ile Val Glu Lys Pro
245 250 255

Ser Asp Leu Pro Ile Glu Glu Ala Glu Trp Phe Lys Arg Leu Thr Gly
260 265 270

Arg Asn Glu Val Ala Ile Ser Ala Arg Asp Tyr Lys Phe Tyr Cys Pro
275 280 285

Arg Arg Lys His Arg Arg Leu Gln Asn Ser Val Ser Ser Ile Asn Gly
290 295 300

Leu Pro Thr Phe Pro Gly Ile Asp Ser Ser Thr Leu Ala Asn Thr Gln
305 310 315 320

Gly Phe Arg Glu Asp Gln Ser Gln Gln His Thr Pro Ser Pro Ser
325 330 335

Lys His His Met Ser Ser Leu Ser His Gln Phe His Gln Ser Ile His
340 345 350

Gln Ser His Gln His Gln Ser Ile Tyr Gln Ser Gln His Ala Ala
355 360 365

Thr His Tyr Pro Ser Gln Asn His Gln Cys Asp Pro Glu Leu Ser His
370 375 380

Thr Gln Met Ala Cys Leu Gln Pro Leu Thr Gly Gly His Val Met Pro
385 390 395 400

Asn Ser Pro Ala Lys Phe Cys Asp Gln Cys Gly Ala Gln Tyr Leu Arg
405 410 415

Glu Thr Ser Lys Phe Cys Ser Glu Cys Gly Ser Lys Arg Leu Gly Ile
 420 425 430

<210> 45

<211> 1617

<212> DNA

<213> *Arabidopsis thaliana*

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<221> CDS

<222> (1)..(1617)

<223> 30945

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aat agc atg tat tta cgt gag acc ata ctt tct agt gaa tct cct agt		96
Asn Ser Met Tyr Leu Arg Glu Thr Ile Leu Ser Ser Glu Ser Pro Ser		
20 25 30		
ctc aac act cag aat atc tca gtg aca gtt gaa atg cca ccc atg ttg		144
Leu Asn Thr Gln Asn Ile Ser Val Thr Val Glu Met Pro Pro Met Leu		
35 40 45		
aaa ccg ttg cat ggg cat ctt ctt aaa cac ttt att gtg ttt tca aat		192
Lys Pro Leu His Gly His Leu Leu Lys His Phe Ile Val Phe Ser Asn		
50 55 60		
att gaa gac cag aac agt atc atc ata ata att cat gct act aac aat		240
Ile Glu Asp Gln Asn Ser Ile Ile Ile His Ala Thr Asn Asn		
65 70 75 80		
tgt cta cag cgt tgc ccg tca gtt act aaa gaa cag tgg gca gtg cca		288
Cys Leu Gln Arg Cys Pro Ser Val Thr Lys Glu Gln Trp Ala Val Pro		
85 90 95		
gcg att ttg tct tct ttg aaa atg gaa gaa aac ctt ttg gcc cag gaa		336
Ala Ile Leu Ser Ser Leu Lys Met Glu Glu Asn Leu Leu Ala Gln Glu		
100 105 110		
agg gcc tgt gtg ttc ctc tcc ttg ctg cat aac ttc tcc atg gtt		384
Arg Ala Cys Val Phe Leu Ser Leu Leu His Asn Phe Ser Met Val		
115 120 125		
cac aca aca aaa act ggg aat act ctg aat gtt gat tct ttc tcc tgc		432
His Thr Thr Lys Thr Gly Asn Thr Leu Asn Val Asp Ser Phe Ser Cys		
130 135 140		

ttg gat tct ttc tca aag cat ata cgt ggt atg gct gat act gaa	480
Leu Asp Ser Phe Ser Lys His Ile Arg Gly Gly Met Ala Asp Thr Glu	
145 150 155 160	
gct gga gtt atg ctt tct gga ttt tcg gaa gaa ctc ctt tgt ctt ctt	528
Ala Gly Val Met Leu Ser Gly Phe Ser Glu Glu Leu Leu Cys Leu Leu	
165 170 175	
cag gac ctc ctt tct ggg cag cgg gta tta ttt tcg gtt aaa tcc tca	576
Gln Asp Leu Leu Ser Gly Gln Arg Val Leu Phe Ser Val Lys Ser Ser	
180 185 190	
gaa aca tgt gaa tct gat tta agc atc cct gtc acc ctg aat gga gaa	624
Glu Thr Cys Glu Ser Asp Leu Ser Ile Pro Val Thr Leu Asn Gly Glu	
195 200 205	
aat gta gct ctc gtc aac aaa atc gct cta act gat caa ttg gtg gcc	672
Asn Val Ala Leu Val Asn Lys Ile Ala Leu Thr Asp Gln Leu Val Ala	
210 215 220	
gga agc gct att ttg gcg gca ata tgt act gca ctt gat cgt att gga	720
Gly Ser Ala Ile Leu Ala Ala Ile Cys Thr Ala Leu Asp Arg Ile Gly	
225 230 235 240	
tat atc tgc gaa gct tcc ttt gaa atc ctg cac aag tac agt cat gag	768
Tyr Ile Cys Glu Ala Ser Phe Glu Ile Leu His Lys Tyr Ser His Glu	
245 250 255	
aaa acc tca gtg cta ctg acc att ctt cac gtt ttt gct tac att gct	816
Lys Thr Ser Val Leu Leu Thr Ile Leu His Val Phe Ala Tyr Ile Ala	
260 265 270	
gga gag aaa atg gtg ttg tct agt gag cat ggc ata tca att gca gtg	864
Gly Glu Lys Met Val Leu Ser Ser Glu His Gly Ile Ser Ile Ala Val	
275 280 285	
ttg aaa tac att gtc atg ttt cta gaa aac aaa cat ttt ggt act gtg	912
Ieu Lys Tyr Ile Val Met Phe Leu Glu Asn Lys His Phe Gly Thr Val	
290 295 300	
gag ggc agt tct cga ttg cac cca ggc aag aac aag tgt cca ttc tca	960
Glu Gly Ser Ser Arg Leu His Pro Gly Lys Asn Lys Cys Pro Phe Ser	
305 310 315 320	
gac agg tct tcc tcg ctg gag gct atg gca tct aag ctc atg gaa att	1008
Asp Arg Ser Ser Ser Leu Glu Ala Met Ala Ser Lys Leu Met Glu Ile	
325 330 335	
ctt cag gaa ttt act gag tct aat act ttg cat aaa agc ttg act ggt	1056
Ieu Gln Glu Phe Thr Glu Ser Asn Thr Leu His Lys Ser Leu Thr Gly	
340 345 350	
tca ttg ggt tct agc cac cta gag aag acc gag ttt agg ccg gca cac	1104
Ser Leu Gly Ser Ser His Leu Glu Lys Thr Glu Phe Arg Pro Ala His	
355 360 365	
aaa gat ttc cag tgt gta ttg acc agg gat caa agt atc aat ctc tgt	1152
Lys Asp Phe Gln Cys Val Leu Thr Arg Asp Gln Ser Ile Asn Leu Cys	
370 375 380	

gac att cta tca ttg gtg gag ctt att gct tgt tat acg gct tgg gat	385	390	395	400	1200
Asp Ile Leu Ser Leu Val Glu Leu Ile Ala Cys Tyr Thr Ala Trp Asp					
tgg act agt gcg aac att gtt gct cca ctg ctt aag atg ctg gga atg	405	410	415		1248
Trp Thr Ser Ala Asn Ile Val Ala Pro Leu Leu Lys Met Leu Gly Met					
cca ttg cca atg aac ctc tct gtt gca atc gtc tcc ctt ctt ggg caa	420	425	430		1296
Pro Leu Pro Met Asn Leu Ser Val Ala Ile Val Ser Leu Leu Gly Gln					
ctt agc agt att gga gtg gat gct ggt ggc tat gaa aac gaa gga atc	435	440	445		1344
Leu Ser Ser Ile Gly Val Asp Ala Gly Gly Tyr Glu Asn Glu Gly Ile					
tca aac ttg aga gtg aaa ctg tca gca ttt cta cag tgt gag acg aca	450	455	460		1392
Ser Asn Leu Arg Val Lys Leu Ser Ala Phe Leu Gln Cys Glu Thr Thr					
cta aag gcc ggt ttt gca gtg cag ata gca act gtg agc tcc ctc ctg	465	470	475	480	1440
Leu Lys Ala Gly Phe Ala Val Gln Ile Ala Thr Val Ser Ser Leu Leu					
aag acg ctg cag ctg aaa ttc cca ata gac ttt caa gac aaa acc acc	485	490	495		1488
Lys Thr Leu Gln Leu Lys Phe Pro Ile Asp Phe Gln Asp Lys Thr Thr					
atg att ccg ggt agt ggc gac caa agc tta tct ggt tca gtc aat gtg	500	505	510		1536
Met Ile Pro Gly Ser Gly Asp Gln Ser Leu Ser Gly Ser Val Asn Val					
gtg acc aag tgg ttg tcg ttg agc aag gaa caa cga gtt ttc gca	515	520	525		1584
Val Thr Lys Trp Leu Ser Leu Leu Ser Lys Glu Gln Arg Val Phe Ala					
ttt gag ttt cta caa acc aat gtt gtt aga tga					1617
Phe Glu Phe Leu Gln Thr Asn Val Val Arg	530	535			

<210> 46

<211> 538

<212> PRT

<213> *Arabidopsis thaliana*

<400> 46

Met Asn Glu Asp Lys Asn Pro Ala Arg Ala Ile Asp Leu Ala Ala Ser	1	5	10	15	
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Asn Ser Met Tyr Leu Arg Glu Thr Ile Leu Ser Ser Glu Ser Pro Ser	20	25	30	
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Leu Asn Thr Gln Asn Ile Ser Val Thr Val Glu Met Pro Pro Met Leu
35 40 45

Lys Pro Leu His Gly His Leu Leu Lys His Phe Ile Val Phe Ser Asn
50 55 60

Ile Glu Asp Gln Asn Ser Ile Ile Ile His Ala Thr Asn Asn
65 70 75 80

Cys Leu Gln Arg Cys Pro Ser Val Thr Lys Glu Gln Trp Ala Val Pro
85 90 95

Ala Ile Leu Ser Ser Leu Lys Met Glu Glu Asn Leu Leu Ala Gln Glu
100 105 110

Arg Ala Cys Val Phe Leu Ser Leu Leu Leu His Asn Phe Ser Met Val
115 120 125

His Thr Thr Lys Thr Gly Asn Thr Leu Asn Val Asp Ser Phe Ser Cys
130 135 140

Leu Asp Ser Phe Ser Lys His Ile Arg Gly Gly Met Ala Asp Thr Glu
145 150 155 160

Ala Gly Val Met Leu Ser Gly Phe Ser Glu Glu Leu Leu Cys Leu Leu
165 170 175

Gln Asp Leu Leu Ser Gly Gln Arg Val Leu Phe Ser Val Lys Ser Ser
180 185 190

Glu Thr Cys Glu Ser Asp Leu Ser Ile Pro Val Thr Leu Asn Gly Glu
195 200 205

Asn Val Ala Leu Val Asn Lys Ile Ala Leu Thr Asp Gln Leu Val Ala
210 215 220

Gly Ser Ala Ile Leu Ala Ala Ile Cys Thr Ala Leu Asp Arg Ile Gly
225 230 235 240

Tyr Ile Cys Glu Ala Ser Phe Glu Ile Leu His Lys Tyr Ser His Glu
245 250 255

Lys Thr Ser Val Leu Leu Thr Ile Leu His Val Phe Ala Tyr Ile Ala
260 265 270

Gly Glu Lys Met Val Leu Ser Ser Glu His Gly Ile Ser Ile Ala Val
275 280 285

Leu Lys Tyr Ile Val Met Phe Leu Glu Asn Lys His Phe Gly Thr Val
290 295 300

Glu Gly Ser Ser Arg Leu His Pro Gly Lys Asn Lys Cys Pro Phe Ser
305 310 315 320

Asp Arg Ser Ser Ser Leu Glu Ala Met Ala Ser Lys Leu Met Glu Ile
325 330 335

Leu Gln Glu Phe Thr Glu Ser Asn Thr Leu His Lys Ser Leu Thr Gly
340 345 350

Ser Leu Gly Ser Ser His Leu Glu Lys Thr Glu Phe Arg Pro Ala His
355 360 365

Lys Asp Phe Gln Cys Val Leu Thr Arg Asp Gln Ser Ile Asn Leu Cys
370 375 380

Asp Ile Leu Ser Leu Val Glu Leu Ile Ala Cys Tyr Thr Ala Trp Asp
385 390 395 400

Trp Thr Ser Ala Asn Ile Val Ala Pro Leu Leu Lys Met Leu Gly Met
405 410 415

Pro Leu Pro Met Asn Leu Ser Val Ala Ile Val Ser Leu Leu Gly Gln
420 425 430

Leu Ser Ser Ile Gly Val Asp Ala Gly Gly Tyr Glu Asn Glu Gly Ile
435 440 445

Ser Asn Leu Arg Val Lys Leu Ser Ala Phe Leu Gln Cys Glu Thr Thr
450 455 460

Leu Lys Ala Gly Phe Ala Val Gln Ile Ala Thr Val Ser Ser Leu Leu
465 470 475 480

Lys Thr Leu Gln Leu Lys Phe Pro Ile Asp Phe Gln Asp Lys Thr Thr
485 490 495

Met Ile Pro Gly Ser Gly Asp Gln Ser Leu Ser Gly Ser Val Asn Val
500 505 510

Val Thr Lys Trp Leu Ser Leu Leu Ser Lys Glu Gln Arg Val Phe Ala
 515 520 525

Phe Glu Phe Leu Gln Thr Asn Val Val Arg
 530 535

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<211> 1332

<212> DNA

<213> *Arabidopsis thaliana*

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<222> (1)..(1332)

<223> 31895

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Met Ser Ile Thr Tyr Ser Ala Ile Ser Ser Thr Val Ser Gly Phe		
1 5 10 15		
tca cca aaa agt gta cct ttt gct att cat agc gta acc agg agg caa		96
Ser Pro Lys Ser Val Pro Phe Ala Ile His Ser Val Thr Arg Arg Gln		
20 25 30		
ttt ctt aat ccc aac acg ttt tat aga ttt ggg ttc tct cct tct ctt		144
Phe Leu Asn Pro Asn Thr Phe Tyr Arg Phe Gly Phe Ser Pro Ser Leu		
35 40 45		
cag gga agt agc att gag ttt agc ctt cag ttg aat tca aga gtt gtg		192
Gln Gly Ser Ser Ile Glu Phe Ser Leu Gln Leu Asn Ser Arg Val Val		
50 55 60		
ctt agt aaa gag cgt cga tct ctg cca tta gtt gtg aga aat gat cgt		240
Leu Ser Lys Glu Arg Arg Ser Leu Pro Leu Val Val Arg Asn Asp Arg		
65 70 75 80		
cct cag aat gaa gac tta cct aag cag tac aca agg cga gag aag aaa		288
Pro Gln Asn Glu Asp Leu Pro Lys Gln Tyr Thr Arg Arg Glu Lys Lys		
85 90 95		
cct ttc cca gtc cct att gtg gac ctg aga cga gct gcg agg gag aga		336
Pro Phe Pro Val Pro Ile Val Asp Leu Arg Arg Ala Ala Arg Glu Arg		
100 105 110		
gtc aag aac aac aaa gac aaa cct aag aga cct cta cct ccg cct aaa		384

Val Lys Asn Asn Lys Asp Lys Pro Lys Arg Pro Leu Pro Pro Pro Lys			
115	120	125	
aat ggt atg gtt gtg aag agc ctt gtg cct ctt gct tat aaa gta tac		432	
Asn Gly Met Val Val Lys Ser Leu Val Pro Leu Ala Tyr Lys Val Tyr			
130	135	140	
aat gca aga atc aga ttg atc aac aat ctc cac cgg ctt atg aaa gtt		480	
Asn Ala Arg Ile Arg Leu Ile Asn Asn Leu His Arg Leu Met Lys Val			
145	150	155	160
gtt cgt gtt aat gct tgt ggg tgg tgc aat gag att cat gtt gga cct		528	
Val Arg Val Asn Ala Cys Gly Trp Cys Asn Glu Ile His Val Gly Pro			
165	170	175	
tat ggg cat cca ttt aag tcg tgt aaa ggt ccc aat act tcc caa agg		576	
Tyr Gly His Pro Phe Lys Ser Cys Lys Gly Pro Asn Thr Ser Gln Arg			
180	185	190	
aaa ggt ctt cat gaa tgg act aac tcg gtt att gag gac gtt att gtt		624	
Lys Gly Leu His Glu Trp Thr Asn Ser Val Ile Glu Asp Val Ile Val			
195	200	205	
cct ctt gaa gcc tat cac ctt ttt gac cgc ctt ggc aag cgt atc cgt		672	
Pro Leu Glu Ala Tyr His Leu Phe Asp Arg Leu Gly Lys Arg Ile Arg			
210	215	220	
cat gat gaa aga ttc tcg att ccc cga gtt cct gct gta gtt gag ctc		720	
His Asp Glu Arg Phe Ser Ile Pro Arg Val Pro Ala Val Val Glu Leu			
225	230	235	240
tgc att cag ggc ggc gtt gaa ata ccc gaa ttt cca gca aaa agg aga		768	
Cys Ile Gln Gly Val Glu Ile Pro Glu Phe Pro Ala Lys Arg Arg			
245	250	255	
aga aaa ccg att atc cgc att ggc aaa agc gag ttt gtt gat gca gat		816	
Arg Lys Pro Ile Ile Arg Ile Gly Lys Ser Glu Phe Val Asp Ala Asp			
260	265	270	
gaa act gaa ttg cct gat cca gag cct cag cct cct cca gtg cca ttg		864	
Glu Thr Glu Leu Pro Asp Pro Glu Pro Gln Pro Pro Pro Val Pro Leu			
275	280	285	
tta act gag tta cct gtc tca gag atc act ccc cca tct agc gaa gaa		912	
Leu Thr Glu Leu Pro Val Ser Glu Ile Thr Pro Pro Ser Ser Glu Glu			
290	295	300	
gaa aca gtc tcc tta gcc gaa gaa aca tta cag gcc tgg gaa gaa atg		960	
Glu Thr Val Ser Leu Ala Glu Glu Thr Leu Gln Ala Trp Glu Glu Met			
305	310	315	320
aga gca gga gcc aaa aag ctg atg agg atg tac agg gtt agg gtc tgt		1008	
Arg Ala Gly Ala Lys Lys Leu Met Arg Met Tyr Arg Val Arg Val Cys			
325	330	335	
ggg tac tgt cca gag gtt cac gta ggt cca acg gga cac aag gcc cag		1056	
Gly Tyr Cys Pro Glu Val His Val Gly Pro Thr Gly His Lys Ala Gln			
340	345	350	
aac tgt ggt gca ttc aag cac caa cag cgg aat ggc cag cat ggt tgg		1104	

Asn Cys Gly Ala Phe Lys His Gln Gln Arg Asn Gly Gln His Gly Trp			
355	360	365	
caa tct gca gta ctt gac gac ttg ata ccg cca aga tat gtt tgg cat			1152
Gln Ser Ala Val Leu Asp Asp Leu Ile Pro Pro Arg Tyr Val Trp His			
370	375	380	
gtt cct gat gtg aat ggg cca ccg atg cag cga gag cta cga agc ttc			1200
Val Pro Asp Val Asn Gly Pro Pro Met Gln Arg Glu Leu Arg Ser Phe			
385	390	395	400
tac ggg caa gca cct gct gtt gtg gag ata tgt gct cag gct ggc gct			1248
Tyr Gly Gln Ala Pro Ala Val Val Glu Ile Cys Ala Gln Ala Gly Ala			
405	410	415	
gtt gta cct gag cat tat aga gct aca atg aga ctg gag gtt gga att			1296
Val Val Pro Glu His Tyr Arg Ala Thr Met Arg Leu Glu Val Gly Ile			
420	425	430	
cct tcg agt gtg aaa gaa gct gag atg gtt gtt tga			1332
Pro Ser Ser Val Lys Glu Ala Glu Met Val Val			
435	440		
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Met Ser Ile Thr Tyr Ser Ala Ile Ser Ser Ser Thr Val Ser Gly Phe			
1	5	10	15
Ser Pro Lys Ser Val Pro Phe Ala Ile His Ser Val Thr Arg Arg Gln			
20	25	30	
Phe Leu Asn Pro Asn Thr Phe Tyr Arg Phe Gly Phe Ser Pro Ser Leu			
35	40	45	
Gln Gly Ser Ser Ile Glu Phe Ser Leu Gln Leu Asn Ser Arg Val Val			
50	55	60	
Leu Ser Lys Glu Arg Arg Ser Leu Pro Leu Val Val Arg Asn Asp Arg			
65	70	75	80
Pro Gln Asn Glu Asp Leu Pro Lys Gln Tyr Thr Arg Arg Glu Lys Lys			
85	90	95	

Pro Phe Pro Val Pro Ile Val Asp Leu Arg Arg Ala Ala Arg Glu Arg
100 105 110

Val Lys Asn Asn Lys Asp Lys Pro Lys Arg Pro Leu Pro Pro Pro Lys
115 120 125

Asn Gly Met Val Val Lys Ser Leu Val Pro Leu Ala Tyr Lys Val Tyr
130 135 140

Asn Ala Arg Ile Arg Leu Ile Asn Asn Leu His Arg Leu Met Lys Val
145 150 155 160

Val Arg Val Asn Ala Cys Gly Trp Cys Asn Glu Ile His Val Gly Pro
165 170 175

Tyr Gly His Pro Phe Lys Ser Cys Lys Gly Pro Asn Thr Ser Gln Arg
180 185 190

Lys Gly Leu His Glu Trp Thr Asn Ser Val Ile Glu Asp Val Ile Val
195 200 205

Pro Leu Glu Ala Tyr His Leu Phe Asp Arg Leu Gly Lys Arg Ile Arg
210 215 220

His Asp Glu Arg Phe Ser Ile Pro Arg Val Pro Ala Val Val Glu Leu
225 230 235 240

Cys Ile Gln Gly Gly Val Glu Ile Pro Glu Phe Pro Ala Lys Arg Arg
245 250 255

Arg Lys Pro Ile Ile Arg Ile Gly Lys Ser Glu Phe Val Asp Ala Asp
260 265 270

Glu Thr Glu Leu Pro Asp Pro Glu Pro Gln Pro Pro Pro Val Pro Leu
275 280 285

Leu Thr Glu Leu Pro Val Ser Glu Ile Thr Pro Pro Ser Ser Glu Glu
290 295 300

Glu Thr Val Ser Leu Ala Glu Glu Thr Leu Gln Ala Trp Glu Glu Met
305 310 315 320

Arg Ala Gly Ala Lys Lys Leu Met Arg Met Tyr Arg Val Arg Val Cys
325 330 335

Gly Tyr Cys Pro Glu Val His Val Gly Pro Thr Gly His Lys Ala Gln
 340 345 350

Asn Cys Gly Ala Phe Lys His Gln Gln Arg Asn Gly Gln His Gly Trp
 355 360 365

Gln Ser Ala Val Leu Asp Asp Leu Ile Pro Pro Arg Tyr Val Trp His
 370 375 380

Val Pro Asp Val Asn Gly Pro Pro Met Gln Arg Glu Leu Arg Ser Phe
 385 390 395 400

Tyr Gly Gln Ala Pro Ala Val Val Glu Ile Cys Ala Gln Ala Gly Ala
 405 410 415

Val Val Pro Glu His Tyr Arg Ala Thr Met Arg Leu Glu Val Gly Ile
 420 425 430

Pro Ser Ser Val Lys Glu Ala Glu Met Val Val
 435 440

<210> 49

<211> 540

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (1)..(540)

<223> 34269

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 Met Leu Ser Ser Ile Val Val Val Val Thr Arg Ile Glu Asn Phe Gln
 1 5 10 15

tgt tgt tgt ttg aga gag atg atg gct gcg aag ctt cag aaa tgg cga 96
 Cys Cys Cys Leu Arg Glu Met Met Ala Ala Lys Leu Gln Lys Trp Arg
 20 25 30

aat ctg gca ggt cgt cta gat ctg atg aat cgg agc ggc gct gtg tcg 144
 Asn Leu Ala Gly Arg Leu Asp Leu Met Asn Arg Ser Gly Ala Val Ser
 35 40 45

acg agg cgg ttc ctg cac gaa ggt cca gat acc gtg gag gag ctt ctc	50	55	60	192
Thr Arg Arg Phe Leu His Glu Gly Pro Asp Thr Val Glu Glu Leu Leu				
gaa aga cat cta gcg aag aaa gag aaa cca ata atc gat cac gat gag	65	70	75	240
Glu Arg His Leu Ala Lys Lys Glu Lys Pro Ile Ile Asp His Asp Glu				
gct gag ttt ctg aat aga cgg cgt ctg acg acg cgc cgg gaa gcg	85	90	95	288
Ala Glu Phe Leu Asn Arg Arg Leu Thr Ser Thr Arg Arg Glu Ala				
ttg agt ttg tac aga gac ata tta cga gcg act cgg ttc ttc acg tgg	100	105	110	336
Leu Ser Leu Tyr Arg Asp Ile Leu Arg Ala Thr Arg Phe Phe Thr Trp				
att gat tcc agg gga aat tta tgg agg gac gtg ttg aga gag aac gcg	115	120	125	384
Ile Asp Ser Arg Gly Asn Leu Trp Arg Asp Val Leu Arg Glu Asn Ala				
agg aag gag ttt gaa gcg gcg cga ttt gag acg gat ccg gag gtt atc	130	135	140	432
Arg Lys Glu Phe Glu Ala Ala Arg Phe Glu Thr Asp Pro Glu Val Ile				
aca agg ctt ctg ata ggt gga agc gac gcc gtt tcg tct gct tta gat	145	150	155	480
Thr Arg Leu Leu Ile Gly Gly Ser Asp Ala Val Ser Ser Ala Leu Asp				
aag ctt gcg gag aag caa aga gag atg att gag aaa caa cgc cgt ggt	165	170	175	528
Lys Leu Ala Glu Lys Gln Arg Glu Met Ile Glu Lys Gln Arg Arg Gly				
gat caa cgc tga				540
Asp Gln Arg				

<210> 50

<211> 179

<212> PRT

<213> *Arabidopsis thaliana*

<400> 50

Met Leu Ser Ser Ile Val Val Val Val Thr Arg Ile Glu Asn Phe Gln	1	5	10	15
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Cys Cys Cys Leu Arg Glu Met Met Ala Ala Lys Leu Gln Lys Trp Arg	20	25	30
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Asn Leu Ala Gly Arg Leu Asp Leu Met Asn Arg Ser Gly Ala Val Ser	35	40	45
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Thr Arg Arg Phe Leu His Glu Gly Pro Asp Thr Val Glu Glu Leu Leu
50 55 60

Glu Arg His Leu Ala Lys Lys Glu Lys Pro Ile Ile Asp His Asp Glu
65 70 75 80

Ala Glu Phe Leu Asn Arg Arg Arg Leu Thr Ser Thr Arg Arg Glu Ala
85 90 95

Leu Ser Leu Tyr Arg Asp Ile Leu Arg Ala Thr Arg Phe Phe Thr Trp
100 105 110

Ile Asp Ser Arg Gly Asn Leu Trp Arg Asp Val Leu Arg Glu Asn Ala
115 120 125

Arg Lys Glu Phe Glu Ala Ala Arg Phe Glu Thr Asp Pro Glu Val Ile
130 135 140

Thr Arg Leu Leu Ile Gly Gly Ser Asp Ala Val Ser Ser Ala Leu Asp
145 150 155 160

Lys Leu Ala Glu Lys Gln Arg Glu Met Ile Glu Lys Gln Arg Arg Gly
165 170 175

Asp Gln Arg

<210> 51

<211> 708

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (1)..(708)

<223> 34540

<400> 51

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48

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1	5	10	15	
tat ttg aaa tcc ctt aaa ctg cag gag aaa tta gtt tca gag aga aaa				96
Tyr Leu Lys Ser Leu Lys Leu Gln Glu Lys Leu Val Ser Glu Arg Lys				
20	25	30		
gct cat cag att cca gat acc ctc ctc tcg ctt cag cat cca cca act				144
Ala His Gln Ile Pro Asp Thr Leu Leu Ser Leu Gln His Pro Pro Thr				
35	40	45		
tat acg ctc gga aag cgt aga acc gat cac aat cta ctt atc cct gaa				192
Tyr Thr Leu Gly Lys Arg Arg Thr Asp His Asn Leu Leu Ile Pro Glu				
50	55	60		
tct gaa ctt aca aaa atc gga gct gaa ctt cat tat act caa aga gga				240
Ser Glu Leu Thr Lys Ile Gly Ala Glu Leu His Tyr Thr Gln Arg Gly				
65	70	75	80	
gga gac atc acc ttc cat ggc cct cat caa gcc atc tta tat ccc atc				288
Gly Asp Ile Thr Phe His Gly Pro His Gln Ala Ile Leu Tyr Pro Ile				
85	90	95		
att tcc tta cgc agc att ggt ttt ggt gct agg aac tac gtg gag aca				336
Ile Ser Leu Arg Ser Ile Gly Phe Gly Ala Arg Asn Tyr Val Glu Thr				
100	105	110		
ttg gag cgg tca atg atc gag ttt gct tcg att tat ggc gtg aaa gct				384
Leu Glu Arg Ser Met Ile Glu Phe Ala Ser Ile Tyr Gly Val Lys Ala				
115	120	125		
cga gca gga aac aaa tgt gag act ggg gtt tgg gtt ggg gat agg aag				432
Arg Ala Gly Asn Lys Cys Glu Thr Gly Val Trp Val Gly Asp Arg Lys				
130	135	140		
atc ggt gct att ggg gtt agg ata tct tct gga atc act agt cat ggt				480
Ile Gly Ala Ile Gly Val Arg Ile Ser Ser Gly Ile Thr Ser His Gly				
145	150	155	160	
ttg gcc tta aat ata gat cct gat atg aag tac ttt gag cac att gtg				528
Leu Ala Leu Asn Ile Asp Pro Asp Met Lys Tyr Phe Glu His Ile Val				
165	170	175		
cct tgt ggg att gct gat aaa gaa gtt aca tct ttg cga aga gag acg				576
Pro Cys Gly Ile Ala Asp Lys Glu Val Thr Ser Leu Arg Arg Glu Thr				
180	185	190		
gat act ctg ctt cct tca gaa gaa gtg att cat gaa cag ttg gtt tct				624
Asp Thr Leu Leu Pro Ser Glu Glu Val Ile His Glu Gln Leu Val Ser				
195	200	205		
tgt tta gcc aaa gcg ttt tct tat gat gat gtt gtc tgg aag gaa gat				672
Cys Leu Ala Lys Ala Phe Ser Tyr Asp Asp Val Val Trp Lys Glu Asp				
210	215	220		
cct tca ctc att ttg gac acc caa gat aaa gaa taa				708
Pro Ser Leu Ile Leu Asp Thr Gln Asp Lys Glu				
225	230	235		

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<211> 235

<212> PRT

<213> *Arabidopsis thaliana*

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Tyr Leu Lys Ser Leu Lys Leu Gln Glu Lys Leu Val Ser Glu Arg Lys
20 25 30

Ala His Gln Ile Pro Asp Thr Leu Leu Ser Leu Gln His Pro Pro Thr
35 40 45

Tyr Thr Leu Gly Lys Arg Arg Thr Asp His Asn Leu Leu Ile Pro Glu
50 55 60

Ser Glu Leu Thr Lys Ile Gly Ala Glu Leu His Tyr Thr Gln Arg Gly
65 70 75 80

Gly Asp Ile Thr Phe His Gly Pro His Gln Ala Ile Leu Tyr Pro Ile
85 90 95

Ile Ser Leu Arg Ser Ile Gly Phe Gly Ala Arg Asn Tyr Val Glu Thr
100 105 110

Leu Glu Arg Ser Met Ile Glu Phe Ala Ser Ile Tyr Gly Val Lys Ala
115 120 125

Arg Ala Gly Asn Lys Cys Glu Thr Gly Val Trp Val Gly Asp Arg Lys
130 135 140

Ile Gly Ala Ile Gly Val Arg Ile Ser Ser Gly Ile Thr Ser His Gly
145 150 155 160

Leu Ala Leu Asn Ile Asp Pro Asp Met Lys Tyr Phe Glu His Ile Val
165 170 175

Pro Cys Gly Ile Ala Asp Lys Glu Val Thr Ser Leu Arg Arg Glu Thr
180 185 190

Asp Thr Leu Leu Pro Ser Glu Glu Val Ile His Glu Gln Leu Val Ser
 195 200 205

Cys Leu Ala Lys Ala Phe Ser Tyr Asp Asp Val Val Trp Lys Glu Asp
 210 215 220

Pro Ser Leu Ile Leu Asp Thr Gln Asp Lys Glu
 225 230 235

<210> 53

<211> 1473

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (1)..(1473)

<223>

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1 5 10 15		
cgt cac acc gcg att ttt cac ggc gga gtt gga gtt aga ttc aaa ttc		96
Arg His Thr Ala Ile Phe His Gly Gly Val Gly Val Arg Phe Lys Phe		
20 25 30		
ctt cgc agc ttt tct cct ctc tca gca aga cga gat aat ccc gat gtc		144
Leu Arg Ser Phe Ser Pro Leu Ser Ala Arg Arg Asp Asn Pro Asp Val		
35 40 45		
tcc aga aaa ccc caa ccg agc aaa aat atg ctc aga gcg aag cac atc		192
Ser Arg Lys Pro Gln Pro Ser Lys Asn Met Leu Arg Ala Lys His Ile		
50 55 60		
ggt aaa aat tac tcc tcc tcc ttg tca cca gtt ctc tcg ccg gag cat		240
Gly Lys Asn Tyr Ser Ser Ser Leu Ser Pro Val Leu Ser Pro Glu His		
65 70 75 80		
aaa cct tcg ctc tta gag tct caa gct att ggt act gtc gca aca gct		288
Lys Pro Ser Leu Leu Glu Ser Gln Ala Ile Gly Thr Val Ala Thr Ala		
85 90 95		
caa gcg aac ttt atg cgc gtc att gtt caa gat gta gct aat tct gtg		336
Gln Ala Asn Phe Met Arg Val Ile Val Gln Asp Val Ala Asn Ser Val		
100 105 110		

acg agt gat gat gat aat gat tct tca aag act ggt gtt gaa ttg ctt	384
Thr Ser Asp Asp Asp Asn Asp Ser Ser Lys Thr Gly Val Glu Leu Leu	
115 120 125	
tgt gtg gtg aga gct gtg ttg aag aaa ata cga agg aga gtt tta gtt	432
Cys Val Val Arg Ala Val Leu Lys Lys Ile Arg Arg Arg Val Leu Val	
130 135 140	
gga gat aag gtt ctt gtt gga tct att gat tgg gtt gat aga aga gga	480
Gly Asp Lys Val Leu Val Gly Ser Ile Asp Trp Val Asp Arg Arg Gly	
145 150 155 160	
atg att gag aat gtg ttt cat cga cgt tcg gag att ttg gat cca cct	528
Met Ile Glu Asn Val Phe His Arg Arg Ser Glu Ile Leu Asp Pro Pro	
165 170 175	
gtt gcg aac gtt gat cat ttg ctt gtt ctt ttc tct ttg gat caa ccg	576
Val Ala Asn Val Asp His Leu Leu Val Leu Phe Ser Leu Asp Gln Pro	
180 185 190	
aaa ctt gag ccg ttt act ctt act agg ttc ttg gtg gaa gct gaa tct	624
Lys Leu Glu Pro Phe Thr Leu Thr Arg Phe Leu Val Glu Ala Glu Ser	
195 200 205	
act cgt att cca tta aca ctt gct ttg aat aaa act gaa ctc att agt	672
Thr Arg Ile Pro Leu Thr Leu Ala Leu Asn Lys Thr Glu Leu Ile Ser	
210 215 220	
gaa gag gaa ttg gaa act tgg aag ata agg ttg cgt gga tgg aac tat	720
Glu Glu Leu Glu Thr Trp Lys Ile Arg Leu Arg Gly Trp Asn Tyr	
225 230 235 240	
gaa cca ttg ttt tgt agt gtg gga act aaa gat gga ctt gat gat att	768
Glu Pro Leu Phe Cys Ser Val Gly Thr Lys Asp Gly Leu Asp Asp Ile	
245 250 255	
gcg ttt gtt ctg aga gat cag act tct gtg att gtt gga cct agt ggt	816
Ala Phe Val Leu Arg Asp Gln Thr Ser Val Ile Val Gly Pro Ser Gly	
260 265 270	
gtt gga aag tcg agt tta atc aac gta ttg agg agt aat cat ggt ggt	864
Val Gly Lys Ser Ser Leu Ile Asn Val Leu Arg Ser Asn His Gly Gly	
275 280 285	
ggt gtg gtg gaa gat gag aat tgg ttt gag cct atg tta ggt aat aag	912
Gly Val Val Glu Asp Glu Asn Trp Phe Glu Pro Met Leu Gly Asn Lys	
290 295 300	
tgg ttt gat gat cag cga gta ggg gaa gtt tcg agt aga agt ggt aga	960
Trp Phe Asp Asp Gln Arg Val Gly Glu Val Ser Ser Arg Ser Gly Arg	
305 310 315 320	
ggt aaa cat aca aca cga aat gta tcg cta ctg ccg gtt tct gaa ggt	1008
Gly Lys His Thr Thr Arg Asn Val Ser Leu Leu Pro Val Ser Glu Gly	
325 330 335	
ggt tac ctc gct gat act cct ggc ttt aac cag cct agt ttg ctg aaa	1056
Gly Tyr Leu Ala Asp Thr Pro Gly Phe Asn Gln Pro Ser Leu Leu Lys	
340 345 350	

gta acg aag cat tca cta gct cac tgt ttt cct gag ata cgg aac atg	355	360	365	1104
Val Thr Lys His Ser Leu Ala His Cys Phe Pro Glu Ile Arg Asn Met				
att gag agc gaa aaa tgt gga ttc aga gac tgc ttg cat att ggg gaa	370	375	380	1152
Ile Glu Ser Glu Lys Cys Gly Phe Arg Asp Cys Leu His Ile Gly Glu				
cca gga tgt gtt gtg aaa ggt gac tgg gaa agg tat cct tac tac tta	385	390	395	1200
Pro Gly Cys Val Val Lys Gly Asp Trp Glu Arg Tyr Pro Tyr Tyr Leu				
caa ttg ctt gat gag atc aga atc agg gaa gaa ttt cag ctt agg act	405	410	415	1248
Gln Leu Leu Asp Glu Ile Arg Ile Arg Glu Glu Phe Gln Leu Arg Thr				
ttt gga acc aaa agg gaa gat gat gtt agg tac aag gtg gga gac atg	420	425	430	1296
Phe Gly Thr Lys Arg Glu Asp Asp Val Arg Tyr Lys Val Gly Asp Met				
ggt gtg aaa cat gct gaa cca cgg tta atg cct aag aag cat agg aga	435	440	445	1344
Gly Val Lys His Ala Glu Pro Arg Leu Met Pro Lys Lys His Arg Arg				
gag tca agg aag aaa acg aaa cag aca atg atc agt gag ctg gat gag	450	455	460	1392
Glu Ser Arg Lys Lys Thr Lys Gln Thr Met Ile Ser Glu Leu Asp Glu				
ttc gaa gat gaa gac agt gat ttg tac ata gag aac gac cca atc gtc	465	470	475	1440
Phe Glu Asp Glu Asp Ser Asp Leu Tyr Ile Glu Asn Asp Pro Ile Val				
caa gcc att gag aat gag aat aaa aga caa tga	485	490		1473
Gln Ala Ile Glu Asn Glu Asn Lys Arg Gln				

<210> 54

<211> 490

<212> PRT

<213> *Arabidopsis thaliana*

<400> 54

Met Gln Thr Phe Ser Ile Ser Leu Leu Arg His Ser Ser Pro Phe Leu				
1	5	10	15	

Arg His Thr Ala Ile Phe His Gly Gly Val Gly Val Arg Phe Lys Phe				
20	25	30		

Leu Arg Ser Phe Ser Pro Leu Ser Ala Arg Arg Asp Asn Pro Asp Val				
35	40	45		

Ser Arg Lys Pro Gln Pro Ser Lys Asn Met Leu Arg Ala Lys His Ile
50 55 60

Gly Lys Asn Tyr Ser Ser Ser Leu Ser Pro Val Leu Ser Pro Glu His
65 70 75 80

Lys Pro Ser Leu Leu Glu Ser Gln Ala Ile Gly Thr Val Ala Thr Ala
85 90 95

Gln Ala Asn Phe Met Arg Val Ile Val Gln Asp Val Ala Asn Ser Val
100 105 110

Thr Ser Asp Asp Asp Asn Asp Ser Ser Lys Thr Gly Val Glu Leu Leu
115 120 125

Cys Val Val Arg Ala Val Leu Lys Lys Ile Arg Arg Arg Val Leu Val
130 135 140

Gly Asp Lys Val Leu Val Gly Ser Ile Asp Trp Val Asp Arg Arg Gly
145 150 155 160

Met Ile Glu Asn Val Phe His Arg Arg Ser Glu Ile Leu Asp Pro Pro
165 170 175

Val Ala Asn Val Asp His Leu Leu Val Leu Phe Ser Leu Asp Gln Pro
180 185 190

Lys Leu Glu Pro Phe Thr Leu Thr Arg Phe Leu Val Glu Ala Glu Ser
195 200 205

Thr Arg Ile Pro Leu Thr Leu Ala Leu Asn Lys Thr Glu Leu Ile Ser
210 215 220

Glu Glu Glu Leu Glu Thr Trp Lys Ile Arg Leu Arg Gly Trp Asn Tyr
225 230 235 240

Glu Pro Leu Phe Cys Ser Val Gly Thr Lys Asp Gly Leu Asp Asp Ile
245 250 255

Ala Phe Val Leu Arg Asp Gln Thr Ser Val Ile Val Gly Pro Ser Gly
260 265 270

Val Gly Lys Ser Ser Leu Ile Asn Val Leu Arg Ser Asn His Gly Gly
275 280 285

Gly Val Val Glu Asp Glu Asn Trp Phe Glu Pro Met Leu Gly Asn Lys
290 295 300

Trp Phe Asp Asp Gln Arg Val Gly Glu Val Ser Ser Arg Ser Gly Arg
305 310 315 320

Gly Lys His Thr Thr Arg Asn Val Ser Leu Leu Pro Val Ser Glu Gly
325 330 335

Gly Tyr Leu Ala Asp Thr Pro Gly Phe Asn Gln Pro Ser Leu Leu Lys
340 345 350

Val Thr Lys His Ser Leu Ala His Cys Phe Pro Glu Ile Arg Asn Met
355 360 365

Ile Glu Ser Glu Lys Cys Gly Phe Arg Asp Cys Leu His Ile Gly Glu
370 375 380

Pro Gly Cys Val Val Lys Gly Asp Trp Glu Arg Tyr Pro Tyr Tyr Leu
385 390 395 400

Gln Leu Leu Asp Glu Ile Arg Glu Glu Phe Gln Leu Arg Thr
405 410 415

Phe Gly Thr Lys Arg Glu Asp Asp Val Arg Tyr Lys Val Gly Asp Met
420 425 430

Gly Val Lys His Ala Glu Pro Arg Leu Met Pro Lys Lys His Arg Arg
435 440 445

Glu Ser Arg Lys Lys Thr Lys Gln Thr Met Ile Ser Glu Leu Asp Glu
450 455 460

Phe Glu Asp Glu Asp Ser Asp Leu Tyr Ile Glu Asn Asp Pro Ile Val
465 470 475 480

Gln Ala Ile Glu Asn Glu Asn Lys Arg Gln
485 490

<210> 55

<211> 897

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(897)

<223> 35154

<400> 55 atg gtg ttt gga caa gta gta ata ggt cct cca gga tcg gga aag acc Met Val Phe Gly Gln Val Val Ile Gly Pro Pro Gly Ser Gly Lys Thr 1 5 10 15	48
act tat tgc aat gga atg tct cag ttc ctc tct cta atg ggc agg aag Thr Tyr Cys Asn Gly Met Ser Gln Phe Leu Ser Leu Met Gly Arg Lys 20 25 30	96
gtt gct att gtt aat ctg gat cct gca aat gat gca tta cct tat gag Val Ala Ile Val Asn Leu Asp Pro Ala Asn Asp Ala Leu Pro Tyr Glu 35 40 45	144
tgt ggt gtg aat ata gaa gaa ttg atc aag tta gaa gat gtt atg tcg Cys Gly Val Asn Ile Glu Glu Leu Ile Lys Leu Glu Asp Val Met Ser 50 55 60	192
gaa cac tcg ctt ggt cct aat gga ggt ctt gta tat tgt atg gag tac Glu His Ser Leu Gly Pro Asn Gly Gly Leu Val Tyr Cys Met Glu Tyr 65 70 75 80	240
ttg gag aaa aac att gac tgg ctg gaa tct aaa cta aag cct ctt ctg Leu Glu Lys Asn Ile Asp Trp Leu Glu Ser Lys Leu Lys Pro Leu Leu 85 90 95	288
aag gat cat tac att ctc ttt gat ttt cct ggc caa gtg gaa ttg ttc Lys Asp His Tyr Ile Leu Phe Asp Phe Pro Gly Gln Val Glu Leu Phe 100 105 110	336
ttc att cat gac agt acc aag aat gtt ctc acg aag ctg att aaa tca Phe Ile His Asp Ser Thr Lys Asn Val Leu Thr Lys Leu Ile Lys Ser 115 120 125	384
ttg aac ctt aga tta act gct gtg caa cta att gat tcc cat cta tgt Leu Asn Leu Arg Leu Thr Ala Val Gln Leu Ile Asp Ser His Leu Cys 130 135 140	432
tgt gat ccc ggg aac tac gta agt tcg cta ctt ctc tcc tta tcc aca Cys Asp Pro Gly Asn Tyr Val Ser Ser Leu Leu Ser Leu Ser Thr 145 150 155 160	480
atg ctt cac atg gaa ctc cca cat gtc aat gta ttg tct aaa atc gat Met Leu His Met Glu Leu Pro His Val Asn Val Leu Ser Lys Ile Asp 165 170 175	528

ctg att gga agc tac ggg aag cta gct ttc aat tta gat ttc tat acc 576
 Leu Ile Gly Ser Tyr Gly Lys Leu Ala Phe Asn Leu Asp Phe Tyr Thr
 180 185 190

gat gtt caa gac ttg tca tac ttg gag cac cat ctt agt caa gat cct 624
 Asp Val Gln Asp Leu Ser Tyr Leu Glu His His Leu Ser Gln Asp Pro
 195 200 205

cgc tct gct aag tac aga aaa cta aca aaa gag cta tgt agt gtc att 672
 Arg Ser Ala Lys Tyr Arg Lys Leu Thr Lys Glu Leu Cys Ser Val Ile
 210 215 220

gaa gat tac agt ctt gtt aat ttt aca acc ttg gat att cag gat aaa 720
 Glu Asp Tyr Ser Leu Val Asn Phe Thr Thr Leu Asp Ile Gln Asp Lys
 225 230 235 240

gaa agt gtt ggg gat cta gta aag ctc atc gac aag agc aat gga tac 768
 Glu Ser Val Gly Asp Leu Val Lys Leu Ile Asp Lys Ser Asn Gly Tyr
 245 250 255

ata ttt gcc ggc att gat gca agt gtg gtt gaa tac agc aag att gca 816
 Ile Phe Ala Gly Ile Asp Ala Ser Val Val Glu Tyr Ser Lys Ile Ala
 260 265 270

att ggt caa act gat tgg gat tat aac aga gtc gca gct gta cag gag 864
 Ile Gly Gln Thr Asp Trp Asp Tyr Asn Arg Val Ala Ala Val Gln Glu
 275 280 285

aag tac atg gaa gat gag gaa ata caa gac tga 897
 Lys Tyr Met Glu Asp Glu Glu Ile Gln Asp
 290 295

<210> 56

<211> 298

<212> PRT

<213> *Arabidopsis thaliana*

<400> 56

Met Val Phe Gly Gln Val Val Ile Gly Pro Pro Gly Ser Gly Lys Thr
 1 5 10 15

Thr Tyr Cys Asn Gly Met Ser Gln Phe Leu Ser Leu Met Gly Arg Lys
 20 25 30

Val Ala Ile Val Asn Leu Asp Pro Ala Asn Asp Ala Leu Pro Tyr Glu
 35 40 45

Cys Gly Val Asn Ile Glu Glu Leu Ile Lys Leu Glu Asp Val Met Ser
 50 55 60

Glu His Ser Leu Gly Pro Asn Gly Gly Leu Val Tyr Cys Met Glu Tyr
65 70 75 80

Leu Glu Lys Asn Ile Asp Trp Leu Glu Ser Lys Leu Lys Pro Leu Leu
85 90 95

Lys Asp His Tyr Ile Leu Phe Asp Phe Pro Gly Gln Val Glu Leu Phe
100 105 110

Phe Ile His Asp Ser Thr Lys Asn Val Leu Thr Lys Leu Ile Lys Ser
115 120 125

Leu Asn Leu Arg Leu Thr Ala Val Gln Leu Ile Asp Ser His Leu Cys
130 135 140

Cys Asp Pro Gly Asn Tyr Val Ser Ser Leu Leu Ser Leu Ser Thr
145 150 155 160

Met Leu His Met Glu Leu Pro His Val Asn Val Leu Ser Lys Ile Asp
165 170 175

Leu Ile Gly Ser Tyr Gly Lys Leu Ala Phe Asn Leu Asp Phe Tyr Thr
180 185 190

Asp Val Gln Asp Leu Ser Tyr Leu Glu His His Leu Ser Gln Asp Pro
195 200 205

Arg Ser Ala Lys Tyr Arg Lys Leu Thr Lys Glu Leu Cys Ser Val Ile
210 215 220

Glu Asp Tyr Ser Leu Val Asn Phe Thr Thr Leu Asp Ile Gln Asp Lys
225 230 235 240

Glu Ser Val Gly Asp Leu Val Lys Leu Ile Asp Lys Ser Asn Gly Tyr
245 250 255

Ile Phe Ala Gly Ile Asp Ala Ser Val Val Glu Tyr Ser Lys Ile Ala
260 265 270

Ile Gly Gln Thr Asp Trp Asp Tyr Asn Arg Val Ala Ala Val Gln Glu
275 280 285

Lys Tyr Met Glu Asp Glu Glu Ile Gln Asp
290 295

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 <223> 35438

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 1 5 10 15
 aag aag aaa tat tcc gaa tac gat gag att aat aag gaa caa gaa gag 96
 Lys Lys Tyr Ser Glu Tyr Asp Glu Ile Asn Lys Glu Gln Glu Glu
 20 25 30
 aaa ttc ctt acc ttt gtt tca gcc tca gag gag ttg atg gaa cat ttg 144
 Lys Phe Leu Thr Phe Val Ser Ala Ser Glu Glu Leu Met Glu His Leu
 35 40 45
 aga ggt gaa aat cag agt tct ctg gag atg gtt gag aag ttg agg aat 192
 Arg Gly Glu Asn Gln Ser Ser Leu Glu Met Val Glu Lys Leu Arg Asn
 50 55 60
 gaa atc att tca atc aga tct ggc agg gac gac aag ttt ctg gag tgt 240
 Glu Ile Ile Ser Ile Arg Ser Gly Arg Asp Asp Lys Phe Leu Glu Cys
 65 70 75 80
 caa aag ctt ctc atg gaa gaa cta aag aac aaa tca ctt tct gaa 288
 Gln Lys Leu Leu Met Glu Glu Leu Lys Asn Lys Ser Leu Ser Glu
 85 90 95
 gaa gtt gtc aag cta aaa gag ctg gtc caa gag gaa cat cct cgc aac 336
 Glu Val Val Lys Leu Lys Glu Leu Val Gln Glu Glu His Pro Arg Asn
 100 105 110
 tat gaa gat caa agt gga aaa aaa caa aag aga aag act cct gaa agt 384
 Tyr Glu Asp Gln Ser Gly Lys Lys Gln Lys Arg Lys Thr Pro Glu Ser
 115 120 125
 gct cga gtt aca acg aga agc atg ata aaa cgt agc aga ctg tca gaa 432
 Ala Arg Val Thr Thr Arg Ser Met Ile Lys Arg Ser Arg Leu Ser Glu
 130 135 140
 gat ttg gtg gaa acg gat atg gta tca cct gac att agc aaa cat cat 480

Asp Leu Val Glu Thr Asp Met Val Ser Pro Asp Ile Ser Lys His His			
145	150	155	160
aaa gca aag gag cct ctc ttg gtt tct cag cca caa tgc tgc aga aca			528
Lys Ala Lys Glu Pro Leu Leu Val Ser Gln Pro Gln Cys Cys Arg Thr			
165	170	175	
acc tac gat gga tca agt agt tct gct agt tgt aca ttt caa gct ctt			576
Thr Tyr Asp Gly Ser Ser Ser Ala Ser Cys Thr Phe Gln Ala Leu			
180	185	190	
ggc aaa cac ttg cta gga atg aaa tta tca act aat aat aag ggc aaa			624
Gly Lys His Leu Leu Gly Met Lys Leu Ser Thr Asn Asn Lys Gly Lys			
195	200	205	
cgc gcc tgc att gta gcc tca cac cca aca acc ggt tta tcc ttc agc			672
Arg Ala Cys Ile Val Ala Ser His Pro Thr Thr Gly Leu Ser Phe Ser			
210	215	220	
cta act ttt ata aat aac cca aat ggt gaa gaa tct gag ctg ctt tac			720
Leu Thr Phe Ile Asn Asn Pro Asn Gly Glu Ser Glu Leu Leu Tyr			
225	230	235	240
aag cct gca tca ctc gga aca ttt caa aga gtg gca ccg gaa tgg atg			768
Lys Pro Ala Ser Leu Gly Thr Phe Gln Arg Val Ala Pro Glu Trp Met			
245	250	255	
aga gaa gtt ata aag ttc agc aca agt atg tgt ccc atc ttc ttt gaa			816
Arg Glu Val Ile Lys Phe Ser Thr Ser Met Cys Pro Ile Phe Phe Glu			
260	265	270	
aga gtc tct cga gtc att aag ctc aat tgt tga			849
Arg Val Ser Arg Val Ile Lys Leu Asn Cys			
275	280		
<210> 58			
<211> 282			
<212> PRT			
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Met Glu Ala Leu Tyr Ala Lys Leu Tyr Asp Lys Tyr Thr Lys Leu Gln			
1 5 10 15			
Lys Lys Lys Tyr Ser Glu Tyr Asp Glu Ile Asn Lys Glu Gln Glu Glu			
20 25 30			
Lys Phe Leu Thr Phe Val Ser Ala Ser Glu Glu Leu Met Glu His Leu			
35 40 45			

Arg Gly Glu Asn Gln Ser Ser Leu Glu Met Val Glu Lys Leu Arg Asn
50 55 60

Glu Ile Ile Ser Ile Arg Ser Gly Arg Asp Asp Lys Phe Leu Glu Cys
65 70 75 80

Gln Lys Leu Leu Met Glu Glu Leu Lys Asn Lys Ser Leu Ser Glu
85 90 95

Glu Val Val Lys Leu Lys Glu Leu Val Gln Glu Glu His Pro Arg Asn
100 105 110

Tyr Glu Asp Gln Ser Gly Lys Lys Gln Lys Arg Lys Thr Pro Glu Ser
115 120 125

Ala Arg Val Thr Thr Arg Ser Met Ile Lys Arg Ser Arg Leu Ser Glu
130 135 140

Asp Leu Val Glu Thr Asp Met Val Ser Pro Asp Ile Ser Lys His His
145 150 155 160

Lys Ala Lys Glu Pro Leu Leu Val Ser Gln Pro Gln Cys Cys Arg Thr
165 170 175

Thr Tyr Asp Gly Ser Ser Ser Ala Ser Cys Thr Phe Gln Ala Leu
180 185 190

Gly Lys His Leu Leu Gly Met Lys Leu Ser Thr Asn Asn Lys Gly Lys
195 200 205

Arg Ala Cys Ile Val Ala Ser His Pro Thr Thr Gly Leu Ser Phe Ser
210 215 220

Leu Thr Phe Ile Asn Asn Pro Asn Gly Glu Ser Glu Leu Leu Tyr
225 230 235 240

Lys Pro Ala Ser Leu Gly Thr Phe Gln Arg Val Ala Pro Glu Trp Met
245 250 255

Arg Glu Val Ile Lys Phe Ser Thr Ser Met Cys Pro Ile Phe Phe Glu
260 265 270

Arg Val Ser Arg Val Ile Lys Leu Asn Cys
275 280

<210> 59
 <211> 1467
 <212> DNA
 <213> *Arabidopsis thaliana*

<220>
 <221> CDS
 <222> (1)..(1467)
 <223> 37351

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atg gaa ttg gat tcg gag aac aaa ttg ttg aag acg ggt ttg gtt ata		48
Met Glu Leu Asp Ser Glu Asn Lys Leu Leu Lys Thr Gly Leu Val Ile		
1 5 10 15		
gtg gcg aca ctt gtt ata gcc aaa ctc atc ttc tct ttc act tct		96
Val Ala Thr Leu Val Ile Ala Lys Leu Ile Phe Ser Phe Phe Thr Ser		
20 25 30		
gat tct aag aag aag cgt ctt cct cct act ctt aaa gct tgg cct cca		144
Asp Ser Lys Lys Lys Arg Leu Pro Pro Thr Leu Lys Ala Trp Pro Pro		
35 40 45		
ttg gtt gga agt ctt atc aaa ttc ttg aaa gga cct att att atg ctt		192
Leu Val Gly Ser Leu Ile Lys Phe Leu Lys Gly Pro Ile Ile Met Leu		
50 55 60		
aga gag gaa tac cct aag ctt gga agt gtg ttt act gtt aat ctt gtt		240
Arg Glu Glu Tyr Pro Lys Leu Gly Ser Val Phe Thr Val Asn Leu Val		
65 70 75 80		
cac aaa aag att act ttt ctt att ggt cct gaa gtc tct gct cat ttt		288
His Lys Lys Ile Thr Phe Leu Ile Gly Pro Glu Val Ser Ala His Phe		
85 90 95		
ttc aaa gct tct gaa tct gat ctt agt cag cag gaa gtg tat cag ttc		336
Phe Lys Ala Ser Glu Ser Asp Leu Ser Gln Gln Glu Val Tyr Gln Phe		
100 105 110		
aat gtc cct act ttt ggt cct gga gtt gtt ttc gat gtt gat tat tct		384
Asn Val Pro Thr Phe Gly Pro Gly Val Val Phe Asp Val Asp Tyr Ser		
115 120 125		
gtt cgt cag gag cag ttt cgg ttc act gag gca ctt aga gtt aac		432
Val Arg Gln Glu Gln Phe Arg Phe Thr Glu Ala Leu Arg Val Asn		
130 135 140		
aag ttg aag ggt tat gtg gat atg atg gtt act gaa gct gag gat tac		480
Lys Leu Lys Gly Tyr Val Asp Met Met Val Thr Glu Ala Glu Asp Tyr		
145 150 155 160		

ttc tct aaa tgg gga gag agt ggt gaa gtt gat att aag gtt gag cta	165	170	175	528
Phe Ser Lys Trp Gly Glu Ser Gly Glu Val Asp Ile Lys Val Glu Leu				
gag agg ctc atc atc ttg act gca agt aga tgt tta ctg ggt cga gaa	180	185	190	576
Glu Arg Leu Ile Ile Leu Thr Ala Ser Arg Cys Leu Leu Gly Arg Glu				
gtt cgt gat cag ctt ttt gat gtc tct gct ttg ttc cat gac ctt	195	200	205	624
Val Arg Asp Gln Leu Phe Asp Asp Val Ser Ala Leu Phe His Asp Leu				
gac aat gga atg ctt ccc atc agt gtt ctc ttc cca tat ctc cca att	210	215	220	672
Asp Asn Gly Met Leu Pro Ile Ser Val Leu Phe Pro Tyr Leu Pro Ile				
cca gct cac cgc cgt cgt gac cgt gcc cga gaa aag ctt tcg gag att	225	230	235	720
Pro Ala His Arg Arg Asp Arg Ala Arg Glu Lys Leu Ser Glu Ile				
ttc gca aaa atc att ggg tcg aga aaa cgc tct gga aaa aca gag aac	245	250	255	768
Phe Ala Lys Ile Ile Gly Ser Arg Lys Arg Ser Gly Lys Thr Glu Asn				
gac atg ctg cag tgt ttc atc gaa tca aag tac aaa gat ggt aga cag	260	265	270	816
Asp Met Leu Gln Cys Phe Ile Glu Ser Lys Tyr Lys Asp Gly Arg Gln				
aca acc gaa tct gaa gtc act ggt ttg ctc att gct gct ctg ttt gca	275	280	285	864
Thr Thr Glu Ser Glu Val Thr Gly Leu Leu Ile Ala Ala Leu Phe Ala				
gga caa cac acg agc tct atc act tcc acc tgg acc ggt gct tat ctg	290	295	300	912
Gly Gln His Thr Ser Ser Ile Thr Ser Thr Trp Thr Gly Ala Tyr Leu				
atg cga tac aaa gag tac ttc tca gct gct ctt gat gag cag aag aac	305	310	315	960
Met Arg Tyr Lys Glu Tyr Phe Ser Ala Ala Leu Asp Glu Gln Lys Asn				
ctg att gcg aaa cat gga gac aag atc gat cat gat atc tta tcc gag	325	330	335	1008
Leu Ile Ala Lys His Gly Asp Lys Ile Asp His Asp Ile Leu Ser Glu				
atg gat gtt ctc tac cgc tgc att aag gaa gcg ttg agg ctt cac cct	340	345	350	1056
Met Asp Val Leu Tyr Arg Cys Ile Lys Glu Ala Leu Arg Leu His Pro				
cca ctc atc atg tta atg aga gcc tcg cac agt gat ttc agc gtg aca	355	360	365	1104
Pro Leu Ile Met Leu Met Arg Ala Ser His Ser Asp Phe Ser Val Thr				
gct cgg gat gga aaa act tac gat atc cca aag ggt cac atc gtt gca	370	375	380	1152
Ala Arg Asp Gly Lys Thr Tyr Asp Ile Pro Lys Gly His Ile Val Ala				
acc tcc cct gca ttt gcc aac cgc tta ccg cac atc ttc aaa gac ccc	385	390	395	1200
Thr Ser Pro Ala Phe Ala Asn Arg Leu Pro His Ile Phe Lys Asp Pro				

gac acc tac gac cca gaa aga ttc tcc cct gga aga gaa gag gac aaa	405	410	415	1248
Asp Thr Tyr Asp Pro Glu Arg Phe Ser Pro Gly Arg Glu Glu Asp Lys				
420	425	430		1296
gcc gca ggg gca ttc tcg tac att gca ttc gga ggg gga agg cac ggg				
Ala Ala Gly Ala Phe Ser Tyr Ile Ala Phe Gly Gly Arg His Gly				
435	440	445		1344
tgc ctt gga gag ccg ttt gct tac ctg cag atc aaa gcc ata tgg agt				
Cys Leu Gly Glu Pro Phe Ala Tyr Leu Gln Ile Lys Ala Ile Trp Ser				
450	455	460		1392
cat ttg ttg agg aac ttc gag ctt gag cta gtt tca ccg ttc cct gag				
His Leu Leu Arg Asn Phe Glu Leu Glu Leu Val Ser Pro Phe Pro Glu				
465	470	475	480	1440
att gac tgg aac gct atg gtg gtt gga gtt aaa ggc aat gtg atg gtg				
Ile Asp Trp Asn Ala Met Val Val Gly Val Lys Gly Asn Val Met Val				
485				
cgt tac aag agg cgc cag ctt tct taa				1467
Arg Tyr Lys Arg Arg Gln Leu Ser				
495				

<210> 60

<211> 488

<212> PRT

<213> *Arabidopsis thaliana*

<400> 60

Met Glu Leu Asp Ser Glu Asn Lys Leu Leu Lys Thr Gly Leu Val Ile				
1	5	10	15	

Val Ala Thr Leu Val Ile Ala Lys Leu Ile Phe Ser Phe Phe Thr Ser				
20	25	30		

Asp Ser Lys Lys Lys Arg Leu Pro Pro Thr Leu Lys Ala Trp Pro Pro				
35	40	45		

Leu Val Gly Ser Leu Ile Lys Phe Leu Lys Gly Pro Ile Ile Met Leu				
50	55	60		

Arg Glu Glu Tyr Pro Lys Leu Gly Ser Val Phe Thr Val Asn Leu Val				
65	70	75	80	

His Lys Lys Ile Thr Phe Leu Ile Gly Pro Glu Val Ser Ala His Phe				
85	90	95		

Phe Lys Ala Ser Glu Ser Asp Leu Ser Gln Gln Glu Val Tyr Gln Phe
100 105 110

Asn Val Pro Thr Phe Gly Pro Gly Val Val Phe Asp Val Asp Tyr Ser
115 120 125

Val Arg Gln Glu Gln Phe Arg Phe Phe Thr Glu Ala Leu Arg Val Asn
130 135 140

Lys Leu Lys Gly Tyr Val Asp Met Met Val Thr Glu Ala Glu Asp Tyr
145 150 155 160

Phe Ser Lys Trp Gly Glu Ser Gly Glu Val Asp Ile Lys Val Glu Leu
165 170 175

Glu Arg Leu Ile Ile Leu Thr Ala Ser Arg Cys Leu Leu Gly Arg Glu
180 185 190

Val Arg Asp Gln Leu Phe Asp Asp Val Ser Ala Leu Phe His Asp Leu
195 200 205

Asp Asn Gly Met Leu Pro Ile Ser Val Leu Phe Pro Tyr Leu Pro Ile
210 215 220

Pro Ala His Arg Arg Asp Arg Ala Arg Glu Lys Leu Ser Glu Ile
225 230 235 240

Phe Ala Lys Ile Ile Gly Ser Arg Lys Arg Ser Gly Lys Thr Glu Asn
245 250 255

Asp Met Leu Gln Cys Phe Ile Glu Ser Lys Tyr Lys Asp Gly Arg Gln
260 265 270

Thr Thr Glu Ser Glu Val Thr Gly Leu Leu Ile Ala Ala Leu Phe Ala
275 280 285

Gly Gln His Thr Ser Ser Ile Thr Ser Thr Trp Thr Gly Ala Tyr Leu
290 295 300

Met Arg Tyr Lys Glu Tyr Phe Ser Ala Ala Leu Asp Glu Gln Lys Asn
305 310 315 320

Leu Ile Ala Lys His Gly Asp Lys Ile Asp His Asp Ile Leu Ser Glu
325 330 335

Met Asp Val Leu Tyr Arg Cys Ile Lys Glu Ala Leu Arg Leu His Pro
340 345 350

Pro Leu Ile Met Leu Met Arg Ala Ser His Ser Asp Phe Ser Val Thr
355 360 365

Ala Arg Asp Gly Lys Thr Tyr Asp Ile Pro Lys Gly His Ile Val Ala
370 375 380

Thr Ser Pro Ala Phe Ala Asn Arg Leu Pro His Ile Phe Lys Asp Pro
385 390 395 400

Asp Thr Tyr Asp Pro Glu Arg Phe Ser Pro Gly Arg Glu Glu Asp Lys
405 410 415

Ala Ala Gly Ala Phe Ser Tyr Ile Ala Phe Gly Gly Arg His Gly
420 425 430

Cys Leu Gly Glu Pro Phe Ala Tyr Leu Gln Ile Lys Ala Ile Trp Ser
435 440 445

His Leu Leu Arg Asn Phe Glu Leu Glu Leu Val Ser Pro Phe Pro Glu
450 455 460

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Ser Ile Asp Pro Glu Pro Asn Trp Asn Phe Glu Ser Leu Val Ala Glu		
20 25 30		
att gct tct gtt gaa aag aag ctc aat ggc ttc tca atg tat cct cag		144
Ile Ala Ser Val Glu Lys Lys Leu Asn Gly Phe Ser Met Tyr Pro Gln		
35 40 45		
cca att act aac aca acc tta cgg atg gga agg aga ggt gga gga ttt		192
Pro Ile Thr Asn Thr Leu Arg Met Gly Arg Arg Gly Gly Phe		
50 55 60		
gta atg cat gtc tca gaa gat gag atg gag agt gac gaa ggt gaa gag		240
Val Met His Val Ser Glu Asp Glu Met Glu Ser Asp Glu Gly Glu Glu		
65 70 75 80		
agt gat gat gag gaa gaa gaa gat cat agt caa atc tgt aca gcg		288
Ser Asp Asp Glu Glu Glu Glu Asp His Ser Gln Ile Cys Thr Ala		
85 90 95		
gga aaa cgt ttt gcc tgt gat gag ctt tac ttg agt gat gaa tct gat		336
Gly Lys Arg Phe Ala Cys Asp Glu Leu Tyr Leu Ser Asp Glu Ser Asp		
100 105 110		
gaa gag ttt gat cat gaa cct gag tat atg atg aat aag ttg ggt ctg		384
Glu Glu Phe Asp His Glu Pro Glu Tyr Met Met Asn Lys Leu Gly Leu		
115 120 125		
gct gag agt gcc cta tat gag gtt atc aac gac cac caa acc gaa atc		432
Ala Glu Ser Ala Leu Tyr Glu Val Ile Asn Asp His Gln Thr Glu Ile		
130 135 140		
aag gac gac att agg aat caa gta tca gtt gtt gaa aca gaa ata atg		480
Lys Asp Asp Ile Arg Asn Gln Val Ser Val Val Glu Thr Glu Ile Met		
145 150 155 160		
aat gag att gaa acg tct ctc tct gcc ata gcc cgg gtt gaa aag tac		528
Asn Glu Ile Glu Thr Ser Leu Ser Ala Ile Ala Arg Val Glu Lys Tyr		
165 170 175		
agt gag act cgg aaa gaa gtt gaa cgg aaa ctt gat ctt caa tat cag		576
Ser Glu Thr Arg Lys Glu Val Glu Arg Lys Leu Asp Leu Gln Tyr Gln		
180 185 190		
cga aaa gtt gct gaa gca ctt gat acc cat ctg act gca gtc caa cgc		624
Arg Lys Val Ala Glu Ala Leu Asp Thr His Leu Thr Ala Val Gln Arg		
195 200 205		
gaa cat aaa att aaa tcg caa ata gaa gaa aga aag ata agg agc gag		672
Glu His Lys Ile Lys Ser Gln Ile Glu Glu Arg Lys Ile Arg Ser Glu		
210 215 220		
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Glu Ala Gln Glu Glu Ala Arg Arg Lys Glu Arg Ala His Gln Glu Glu			
225	230	235	240
aaa ata cgt caa gaa aaa gct cgc gca gag gct caa atg cta gca aaa			768
Lys Ile Arg Gln Glu Lys Ala Arg Ala Glu Ala Gln Met Leu Ala Lys			
245	250	255	
atc aga gct gaa gaa gaa aag aaa gaa gtt gag aga aag gca gcc aga			816
Ile Arg Ala Glu Glu Lys Lys Glu Val Glu Arg Lys Ala Ala Arg			
260	265	270	
gaa gta gct gaa aaa gaa gta gca gat cgc aaa gct gcc gaa caa aaa			864
Glu Val Ala Glu Lys Glu Val Ala Asp Arg Lys Ala Ala Glu Gln Lys			
275	280	285	
ctt gcg gaa cag aag gct gtg ata gag agt gtt acg ggg agt tca gct			912
Leu Ala Glu Gln Lys Ala Val Ile Glu Ser Val Thr Gly Ser Ser Ala			
290	295	300	
aca tca aat gct caa gct ggg ggt aat tca atc cga gct gca gaa agt			960
Thr Ser Asn Ala Gln Ala Gly Gly Asn Ser Ile Arg Ala Ala Glu Ser			
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gct ttg ata ttg gag aac cac aga ttg aaa aag ctc gaa gaa cta gaa			1008
Ala Leu Ile Leu Glu Asn His Arg Leu Lys Lys Leu Glu Glu Leu Glu			
325	330	335	
aca acg aac caa tcg ctt aag tca cgt tca aat gaa aac ttt agc agt			1056
Thr Thr Asn Gln Ser Leu Lys Ser Arg Ser Asn Glu Asn Phe Ser Ser			
340	345	350	
ttt gag aag cat att gga aga gtg ata agg caa ata agt ggg aca aag			1104
Phe Glu Lys His Ile Gly Arg Val Ile Arg Gln Ile Ser Gly Thr Lys			
355	360	365	
gat agt gta agt ggg aaa atc aat gat att gtg aaa ata ttt aaa gac			1152
Asp Ser Val Ser Gly Lys Ile Asn Asp Ile Val Lys Ile Phe Lys Asp			
370	375	380	
cct cgt tgt ccg gta tcc ata agt att gca gct ttt gca aag aag atg			1200
Pro Arg Cys Pro Val Ser Ile Ser Ile Ala Ala Phe Ala Lys Lys Met			
385	390	395	400
gtc acc act aag gaa aaa cca aac cct ttt gca tgc agc tat gtc att			1248
Val Thr Thr Lys Glu Lys Pro Asn Pro Phe Ala Cys Ser Tyr Val Ile			
405	410	415	
gtt tac atc aac tca cag ttt ccc caa gtt atg gat att ctt ctc gcg			1296
Val Tyr Ile Asn Ser Gln Phe Pro Gln Val Met Asp Ile Leu Leu Ala			
420	425	430	
gaa ttc cac aaa gct tgc att tac act gtc cca aag cat att gta aac			1344
Glu Phe His Lys Ala Cys Ile Tyr Thr Val Pro Lys His Ile Val Asn			
435	440	445	
tca cag tca gct tgg gat tca gac gca tat gaa cgc cta gat tct ata			1392
Ser Gln Ser Ala Trp Asp Ser Asp Ala Tyr Glu Arg Leu Asp Ser Ile			
450	455	460	
atg agg ctc tac ggt gca ctt gtt cag acc gat atc cgc gtt ggc aat			1440

Met Arg Leu Tyr Gly Ala Leu Val Gln Thr Asp Ile Arg Val Gly Asn				
465	470	475	480	
gct act aac gtt cat ggg ata gaa cat gga tgg gct tgg tta gcc cg				1488
Ala Thr Asn Val His Gly Ile Glu His Gly Trp Ala Trp Leu Ala Arg				
485	490	495		
ttc ctt aac aaa atc cca gcc aac aga gcc act gcg aca gcc ttg aac				1536
Phe Leu Asn Lys Ile Pro Ala Asn Arg Ala Thr Ala Thr Ala Leu Asn				
500	505	510		
tcc ttt ctc cag acg gct ggg ttt ggt ctt cat cag agg tac aaa tct				1584
Ser Phe Leu Gln Thr Ala Gly Phe Gly Leu His Gln Arg Tyr Lys Ser				
515	520	525		
cag ttt ctg aag gtt gtg aat gtt gtg aga gag cat ttc ttg cag aaa				1632
Gln Phe Leu Lys Val Val Asn Val Val Arg Glu His Phe Leu Gln Lys				
530	535	540		
ttg cgg gcg aag aag gac acg tcg gat cta ctt gtg atc ata gcc gaa				1680
Leu Arg Ala Lys Lys Asp Thr Ser Asp Leu Leu Val Ile Ile Ala Glu				
545	550	555	560	
atc aca gcg tac tta gat gac cgg atg tat ctc aag gaa cct gaa gga				1728
Ile Thr Ala Tyr Leu Asp Asp Arg Met Tyr Leu Lys Glu Pro Glu Gly				
565	570	575		
aga gct atg aag acg act agt acc ttg tcc tct gaa ctt act gct gaa				1776
Arg Ala Met Lys Thr Thr Ser Thr Leu Ser Ser Glu Leu Thr Ala Glu				
580	585	590		
tta aat cag ccg aac tac aat cag aat tac cag agg aat gat tac aga				1824
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Ile Ala Ser Val Glu Lys Lys Leu Asn Gly Phe Ser Met Tyr Pro Gln
35 40 45

Pro Ile Thr Asn Thr Thr Leu Arg Met Gly Arg Arg Gly Gly Phe
50 55 60

Val Met His Val Ser Glu Asp Glu Met Glu Ser Asp Glu Gly Glu Glu
65 70 75 80

Ser Asp Asp Glu Glu Glu Asp His Ser Gln Ile Cys Thr Ala
85 90 95

Gly Lys Arg Phe Ala Cys Asp Glu Leu Tyr Leu Ser Asp Glu Ser Asp
100 105 110

Glu Glu Phe Asp His Glu Pro Glu Tyr Met Met Asn Lys Leu Gly Leu
115 120 125

Ala Glu Ser Ala Leu Tyr Glu Val Ile Asn Asp His Gln Thr Glu Ile
130 135 140

Lys Asp Asp Ile Arg Asn Gln Val Ser Val Val Glu Thr Glu Ile Met
145 150 155 160

Asn Glu Ile Glu Thr Ser Leu Ser Ala Ile Ala Arg Val Glu Lys Tyr
165 170 175

Ser Glu Thr Arg Lys Glu Val Glu Arg Lys Leu Asp Leu Gln Tyr Gln
180 185 190

Arg Lys Val Ala Glu Ala Leu Asp Thr His Leu Thr Ala Val Gln Arg
195 200 205

Glu His Lys Ile Lys Ser Gln Ile Glu Glu Arg Lys Ile Arg Ser Glu
210 215 220

Glu Ala Gln Glu Glu Ala Arg Arg Lys Glu Arg Ala His Gln Glu Glu
225 230 235 240

Lys Ile Arg Gln Glu Lys Ala Arg Ala Glu Ala Gln Met Leu Ala Lys
245 250 255

Ile Arg Ala Glu Glu Lys Lys Glu Val Glu Arg Lys Ala Ala Arg
260 265 270

Glu Val Ala Glu Lys Glu Val Ala Asp Arg Lys Ala Ala Glu Gln Lys
275 280 285

Leu Ala Glu Gln Lys Ala Val Ile Glu Ser Val Thr Gly Ser Ser Ala
290 295 300

Thr Ser Asn Ala Gln Ala Gly Gly Asn Ser Ile Arg Ala Ala Glu Ser
305 310 315 320

Ala Leu Ile Leu Glu Asn His Arg Leu Lys Lys Leu Glu Glu Leu Glu
325 330 335

Thr Thr Asn Gln Ser Leu Lys Ser Arg Ser Asn Glu Asn Phe Ser Ser
340 345 350

Phe Glu Lys His Ile Gly Arg Val Ile Arg Gln Ile Ser Gly Thr Lys
355 360 365

Asp Ser Val Ser Gly Lys Ile Asn Asp Ile Val Lys Ile Phe Lys Asp
370 375 380

Pro Arg Cys Pro Val Ser Ile Ser Ile Ala Ala Phe Ala Lys Lys Met
385 390 395 400

Val Thr Thr Lys Glu Lys Pro Asn Pro Phe Ala Cys Ser Tyr Val Ile
405 410 415

Val Tyr Ile Asn Ser Gln Phe Pro Gln Val Met Asp Ile Leu Leu Ala
420 425 430

Glu Phe His Lys Ala Cys Ile Tyr Thr Val Pro Lys His Ile Val Asn
435 440 445

Ser Gln Ser Ala Trp Asp Ser Asp Ala Tyr Glu Arg Leu Asp Ser Ile
450 455 460

Met Arg Leu Tyr Gly Ala Leu Val Gln Thr Asp Ile Arg Val Gly Asn
465 470 475 480

Ala Thr Asn Val His Gly Ile Glu His Gly Trp Ala Trp Leu Ala Arg
485 490 495

Phe Leu Asn Lys Ile Pro Ala Asn Arg Ala Thr Ala Thr Ala Leu Asn
500 505 510

Ser Phe Leu Gln Thr Ala Gly Phe Gly Leu His Gln Arg Tyr Lys Ser
 515 520 525

Gln Phe Leu Lys Val Val Asn Val Val Arg Glu His Phe Leu Gln Lys
 530 535 540

Leu Arg Ala Lys Lys Asp Thr Ser Asp Leu Leu Val Ile Ile Ala Glu
 545 550 555 560

Ile Thr Ala Tyr Leu Asp Asp Arg Met Tyr Leu Lys Glu Pro Glu Gly
 565 570 575

Arg Ala Met Lys Thr Thr Ser Thr Leu Ser Ser Glu Leu Thr Ala Glu
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tct tct ttc aaa act tct tct tct tca ttt tct ccg aag ctt ctt 96
 Ser Ser Phe Lys Thr Ser Ser Ser Ser Phe Ser Pro Lys Leu Leu
 20 25 30

cga ccc ctc tta agc ttt tcc gtc aaa gct tcc aga aag caa gta gag 144
 Arg Pro Leu Leu Ser Phe Ser Val Lys Ala Ser Arg Lys Gln Val Glu
 35 40 45

ata gtg ttt gat cct gat gag agg ctt aat aag ata ggt gat gat gtt Ile Val Phe Asp Pro Asp Glu Arg Leu Asn Lys Ile Gly Asp Asp Val 50	55	60	192	
gac aaa gaa gct cct ttg tcc agg ctt aag ctc ttc tca cct tgc aag Asp Lys Glu Ala Pro Leu Ser Arg Leu Lys Leu Phe Ser Pro Cys Lys 65	70	75	80	240
atc aat gtt ttc ttg agg atc acc gga aag cga gaa gat ggg ttt cat Ile Asn Val Phe Leu Arg Ile Thr Gly Lys Arg Glu Asp Gly Phe His 85	90	95	288	
gat tta gcc tct ttg ttt cat gtg att agc tta gga gac act att aaa Asp Leu Ala Ser Leu Phe His Val Ile Ser Leu Gly Asp Thr Ile Lys 100	105	110	336	
ttc tca ttg tca cca tca aag tct aaa gat cgt ttg tct act aac gtt Phe Ser Leu Ser Pro Ser Lys Ser Lys Asp Arg Leu Ser Thr Asn Val 115	120	125	384	
caa gga gtc cct gtt gat ggg aga aat ctg att ata aaa gca ctt aac Gln Gly Val Pro Val Asp Gly Arg Asn Leu Ile Ile Lys Ala Leu Asn 130	135	140	432	
ctt tac agg aag aaa act ggt agt aac aga ttc ttc tgg att cat tta Leu Tyr Arg Lys Lys Thr Gly Ser Asn Arg Phe Phe Trp Ile His Leu 145	150	155	160	480
gat aag aag gtg cct acc ggg gct gga ctc ggt ggt gga agt agt aat Asp Lys Lys Val Pro Thr Gly Ala Gly Leu Gly Gly Ser Ser Asn 165	170	175	528	
gct gca act gca ctc tgg gcg gca aat gag ctc aat gga ggt ctt gtc Ala Ala Thr Ala Leu Trp Ala Ala Asn Glu Leu Asn Gly Gly Leu Val 180	185	190	576	
act gag aac gaa ctc cag gat tgg tca agt gaa att ggg tca gat att Thr Glu Asn Glu Leu Gln Asp Trp Ser Ser Glu Ile Gly Ser Asp Ile 195	200	205	624	
cct ttc ttc ttc tcg cat gga gct gcc tat tgt acc ggg aga ggt gag Pro Phe Phe Ser His Gly Ala Ala Tyr Cys Thr Gly Arg Gly Glu 210	215	220	672	
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ctc ata aag ccc cga gaa gca tgt tcc act gct gaa gtt tac aaa cgt Leu Ile Lys Pro Arg Glu Ala Cys Ser Thr Ala Glu Val Tyr Lys Arg 245	250	255	768	
ctt cgt tta gat cag acg agc aat att aat ccc ttg aca tta cta gag Leu Arg Leu Asp Gln Thr Ser Asn Ile Asn Pro Leu Thr Leu Leu Glu 260	265	270	816	
aat gtg acc agc aat ggt gtg tct caa agc ata tgc gta aac gat ttg Asn Val Thr Ser Asn Gly Val Ser Gln Ser Ile Cys Val Asn Asp Leu 275	280	285	864	

gaa ccg cca gcg ttt tca gtt ctt cca tct cta aaa cgc ttg aag caa 912
 Glu Pro Pro Ala Phe Ser Val Leu Pro Ser Leu Lys Arg Leu Lys Gln
 290 295 300

cgg ata ata gca tct gga cgt ggg gaa tac gat gct gtg ttt atg tct 960
 Arg Ile Ile Ala Ser Gly Arg Gly Glu Tyr Asp Ala Val Phe Met Ser
 305 310 315 320

ggg agt gga agc act att atc ggt att ggt tca cca gat cct cct caa 1008
 Gly Ser Gly Ser Thr Ile Ile Gly Ile Gly Ser Pro Asp Pro Pro Gln
 325 330 335

ttt ata tat gat gat gaa gaa tac aag aac gtg ttc ttg tct gaa gca 1056
 Phe Ile Tyr Asp Asp Glu Glu Tyr Lys Asn Val Phe Leu Ser Glu Ala
 340 345 350

aac ttt atg acg cgt gag gct aat gaa tgg tac aaa gaa cct gct tot 1104
 Asn Phe Met Thr Arg Glu Ala Asn Glu Trp Tyr Lys Glu Pro Ala Ser
 355 360 365

gca aat gct act acc tca tcc gcc gaa tct cgc atg gat ttc caa tga 1152
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Arg Pro Leu Leu Ser Phe Ser Val Lys Ala Ser Arg Lys Gln Val Glu
 35 40 45

Ile Val Phe Asp Pro Asp Glu Arg Leu Asn Lys Ile Gly Asp Asp Val
 50 55 60

Asp Lys Glu Ala Pro Leu Ser Arg Leu Lys Leu Phe Ser Pro Cys Lys
 65 70 75 80

Ile Asn Val Phe Leu Arg Ile Thr Gly Lys Arg Glu Asp Gly Phe His
 85 90 95

Asp Leu Ala Ser Leu Phe His Val Ile Ser Leu Gly Asp Thr Ile Lys
100 105 110

Phe Ser Leu Ser Pro Ser Lys Ser Lys Asp Arg Leu Ser Thr Asn Val
115 120 125

Gln Gly Val Pro Val Asp Gly Arg Asn Leu Ile Ile Lys Ala Leu Asn
130 135 140

Leu Tyr Arg Lys Lys Thr Gly Ser Asn Arg Phe Phe Trp Ile His Leu
145 150 155 160

Asp Lys Lys Val Pro Thr Gly Ala Gly Leu Gly Gly Ser Ser Asn
165 170 175

Ala Ala Thr Ala Leu Trp Ala Ala Asn Glu Leu Asn Gly Gly Leu Val
180 185 190

Thr Glu Asn Glu Leu Gln Asp Trp Ser Ser Glu Ile Gly Ser Asp Ile
195 200 205

Pro Phe Phe Ser His Gly Ala Ala Tyr Cys Thr Gly Arg Gly Glu
210 215 220

Ile Val Gln Asp Leu Pro Pro Pro Phe Pro Leu Asp Leu Pro Met Val
225 230 235 240

Leu Ile Lys Pro Arg Glu Ala Cys Ser Thr Ala Glu Val Tyr Lys Arg
245 250 255

Leu Arg Leu Asp Gln Thr Ser Asn Ile Asn Pro Leu Thr Leu Leu Glu
260 265 270

Asn Val Thr Ser Asn Gly Val Ser Gln Ser Ile Cys Val Asn Asp Leu
275 280 285

Glu Pro Pro Ala Phe Ser Val Leu Pro Ser Leu Lys Arg Leu Lys Gln
290 295 300

Arg Ile Ile Ala Ser Gly Arg Gly Glu Tyr Asp Ala Val Phe Met Ser
305 310 315 320

Gly Ser Gly Ser Thr Ile Ile Gly Ile Gly Ser Pro Asp Pro Pro Gln
325 330 335

Phe Ile Tyr Asp Asp Glu Glu Tyr Lys Asn Val Phe Leu Ser Glu Ala
 340 345 350

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 355 360 365

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 Ala Glu Trp Asp Ser His Ala Gln Thr Trp Ile Gly Trp Pro Glu Arg
 20 25 30

caa gat aac tgg cgg cac aac gct tta ccc gca caa cga gtg ttt gca 144
 Gln Asp Asn Trp Arg His Asn Ala Leu Pro Ala Gln Arg Val Phe Ala
 35 40 45

gat gtt gca aag gcc atc tca aag ttc gag cct gtc act gtc tgt gct 192
 Asp Val Ala Lys Ala Ile Ser Lys Phe Glu Pro Val Thr Val Cys Ala
 50 55 60

agc cct gct cag tgg gaa aat gca agg aaa cag ctt cca gag gat ata 240
 Ser Pro Ala Gln Trp Glu Asn Ala Arg Lys Gln Leu Pro Glu Asp Ile
 65 70 75 80

aga gtt gtt gag atg agc atg aat gat tct tgg ttc cgc gac tct gga 288
 Arg Val Val Glu Met Ser Met Asn Asp Ser Trp Phe Arg Asp Ser Gly
 85 90 95

cca act ttc att gta cgg aaa aga cca gta aag ctc agt tct ctt aac 336

Pro Thr Phe Ile Val Arg Lys Arg Pro Val Lys Leu Ser Ser Leu Asn			
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cga aac att gct ggg atc gac tgg aat ttc aat gcc tgg gga gga gct			384
Arg Asn Ile Ala Gly Ile Asp Trp Asn Phe Asn Ala Trp Gly Gly Ala			
115	120	125	
aat gat ggc tgt tac aat gat tgg agt cat gac ctt tta gtt tca cga			432
Asn Asp Gly Cys Tyr Asn Asp Trp Ser His Asp Leu Leu Val Ser Arg			
130	135	140	
aag att ctc gct ttg gaa cga att cca aga ttt caa cat tcg atg att			480
Lys Ile Leu Ala Leu Glu Arg Ile Pro Arg Phe Gln His Ser Met Ile			
145	150	155	160
ctt gaa gga ggc agc atc cat gtc gat ggg gaa gga acc tgc ctt gtc			528
Leu Glu Gly Ser Ile His Val Asp Gly Glu Gly Thr Cys Leu Val			
165	170	175	
aca gaa gag tgt ctc ttg aac aaa aac cga aac cct cat atg agt aaa			576
Thr Glu Glu Cys Leu Leu Asn Lys Asn Arg Asn Pro His Met Ser Lys			
180	185	190	
gag caa ata gag gaa ctt aag aag tac ctc gga gta caa tca ttt			624
Glu Gln Ile Glu Glu Leu Lys Lys Tyr Leu Gly Val Gln Ser Phe			
195	200	205	
atc tgg ctt cct cgt ggt ctt tac ggg gat gag gac aca aat ggt cac			672
Ile Trp Leu Pro Arg Gly Leu Tyr Gly Asp Glu Asp Thr Asn Gly His			
210	215	220	
att gat aac atg tgc tgc ttc gct aga ccg gga gtt gtg tta ttg tct			720
Ile Asp Asn Met Cys Cys Phe Ala Arg Pro Gly Val Val Leu Leu Ser			
225	230	235	240
tgg aca gac gat gaa acc gat cct caa tac gaa agg tct gtg gaa gct			768
Trp Thr Asp Asp Glu Thr Asp Pro Gln Tyr Glu Arg Ser Val Glu Ala			
245	250	255	
ctt tcg gtt ttg tcg aat tcg att gat gct cgt gga agg aag att caa			816
Leu Ser Val Leu Ser Asn Ser Ile Asp Ala Arg Gly Arg Lys Ile Gln			
260	265	270	
gtc att aaa ctt tat atc ccg gaa ccc ctt tat atg act gaa gaa gaa			864
Val Ile Lys Leu Tyr Ile Pro Glu Pro Leu Tyr Met Thr Glu Glu Glu			
275	280	285	
tcg tct gga atc act cag gat ggt gaa gct ata cca aga ctt gca ggg			912
Ser Ser Gly Ile Thr Gln Asp Gly Glu Ala Ile Pro Arg Leu Ala Gly			
290	295	300	
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Thr Arg Leu Ala Ala Ser Tyr Val Asn Phe Tyr Ile Ala Asn Gly Gly			
305	310	315	320
ata atc gct cca caa ttc ggt gat cca ata cgt gat aaa gaa gcg att			1008
Ile Ile Ala Pro Gln Phe Gly Asp Pro Ile Arg Asp Lys Glu Ala Ile			
325	330	335	
cgt gtc ctc tcg gat aca ttt cct cat cac tcg gtt gtg gga atc gag			1056

Arg Val Leu Ser Asp Thr Phe Pro His His Ser Val Val Gly Ile Glu
340 345 350

aat gca aga gag atc gtt ctt gct gga gga aac att cat tgt ata acg 1104
Asn Ala Arg Glu Ile Val Leu Ala Gly Gly Asn Ile His Cys Ile Thr
355 360 365

cag cag cag ccg gcg gag cct act tcc gtc gcc gaa aat ggc cac tga 1152
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370 375 380

<210> 66

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<213> *Arabidopsis thaliana*

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Gln Asp Asn Trp Arg His Asn Ala Leu Pro Ala Gln Arg Val Phe Ala
35 40 45

Asp Val Ala Lys Ala Ile Ser Lys Phe Glu Pro Val Thr Val Cys Ala
50 55 60

Ser Pro Ala Gln Trp Glu Asn Ala Arg Lys Gln Leu Pro Glu Asp Ile
65 70 75 80

Arg Val Val Glu Met Ser Met Asn Asp Ser Trp Phe Arg Asp Ser Gly
85 90 95

Pro Thr Phe Ile Val Arg Lys Arg Pro Val Lys Leu Ser Ser Leu Asn
100 105 110

Arg Asn Ile Ala Gly Ile Asp Trp Asn Phe Asn Ala Trp Gly Gly Ala
115 120 125

Asn Asp Gly Cys Tyr Asn Asp Trp Ser His Asp Leu Leu Val Ser Arg
130 135 140

Lys Ile Leu Ala Leu Glu Arg Ile Pro Arg Phe Gln His Ser Met Ile
145 150 155 160

Leu Glu Gly Gly Ser Ile His Val Asp Gly Glu Gly Thr Cys Leu Val
165 170 175

Thr Glu Glu Cys Leu Leu Asn Lys Asn Arg Asn Pro His Met Ser Lys
180 185 190

Glu Gln Ile Glu Glu Leu Lys Lys Tyr Leu Gly Val Gln Ser Phe
195 200 205

Ile Trp Leu Pro Arg Gly Leu Tyr Gly Asp Glu Asp Thr Asn Gly His
210 215 220

Ile Asp Asn Met Cys Cys Phe Ala Arg Pro Gly Val Val Leu Leu Ser
225 230 235 240

Trp Thr Asp Asp Glu Thr Asp Pro Gln Tyr Glu Arg Ser Val Glu Ala
245 250 255

Leu Ser Val Leu Ser Asn Ser Ile Asp Ala Arg Gly Arg Lys Ile Gln
260 265 270

Val Ile Lys Leu Tyr Ile Pro Glu Pro Leu Tyr Met Thr Glu Glu Glu
275 280 285

Ser Ser Gly Ile Thr Gln Asp Gly Glu Ala Ile Pro Arg Leu Ala Gly
290 295 300

Thr Arg Leu Ala Ala Ser Tyr Val Asn Phe Tyr Ile Ala Asn Gly Gly
305 310 315 320

Ile Ile Ala Pro Gln Phe Gly Asp Pro Ile Arg Asp Lys Glu Ala Ile
325 330 335

Arg Val Leu Ser Asp Thr Phe Pro His His Ser Val Val Gly Ile Glu
340 345 350

Asn Ala Arg Glu Ile Val Leu Ala Gly Gly Asn Ile His Cys Ile Thr
355 360 365

Gln Gln Gln Pro Ala Glu Pro Thr Ser Val Ala Glu Asn Gly His
370 375 380

<210> 67
 <211> 1935
 <212> DNA
 <213> *Arabidopsis thaliana*

<220>
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 <222> (1)..(1935)
 <223> 46250

<400> 67
 atg gct agt ctt ctt cga tcc tta atc ctt ttg cta atc gtg caa tca 48
 Met Ala Ser Leu Leu Arg Ser Leu Ile Leu Leu Leu Ile Val Gln Ser
 1 5 10 15
 ttt ttg gtt gcg atc gct ttc ggg tcg aaa gaa gtt gaa gaa ttc agc 96
 Phe Leu Val Ala Ile Ala Phe Gly Ser Lys Glu Val Glu Glu Phe Ser
 20 25 30
 gag gca ttg ctc ttg aag cct tta cct gat cga aaa gtt tta gct cac 144
 Glu Ala Leu Leu Lys Pro Leu Pro Asp Arg Lys Val Leu Ala His
 35 40 45
 ttc cac ttc gag aac cga gct cct ccg tca aac tcc cat ggc cgc cat 192
 Phe His Phe Glu Asn Arg Ala Pro Pro Ser Asn Ser His Gly Arg His
 50 55 60
 cac cat ctc ttc ccg aaa gct att tct cag ttg gtt cag aag ttt cgg 240
 His His Leu Phe Pro Lys Ala Ile Ser Gln Leu Val Gln Lys Phe Arg
 65 70 75 80
 gtc aag gag atg gag tta tct ttt act cag ggt cga tgg aac cat gaa 288
 Val Lys Glu Met Glu Leu Ser Phe Thr Gln Gly Arg Trp Asn His Glu
 85 90 95
 cat tgg gga gga ttt gac cct cta tca agt atg aat gcg aag cct gtt 336
 His Trp Gly Gly Phe Asp Pro Leu Ser Ser Met Asn Ala Lys Pro Val
 100 105 110
 ggt gtg gag ctg tgg gct gtg ttt gat gtt cct cag tct cag gtt gat 384
 Gly Val Glu Leu Trp Ala Val Phe Asp Val Pro Gln Ser Gln Val Asp
 115 120 125
 act tct tgg aag aac tta act cat gca ctg tca ggg ctt ttc tgt gct 432
 Thr Ser Trp Lys Asn Leu Thr His Ala Leu Ser Gly Leu Phe Cys Ala
 130 135 140
 tcc atc aat ttt cta gaa tct tcc act tca tat gct gct cct aca tgg 480
 Ser Ile Asn Phe Leu Glu Ser Ser Thr Ser Tyr Ala Ala Pro Thr Trp
 145 150 155 160

gga ttt gga ccc aat tct gac aag ctg agg tat ggt tca ctg cca cgt Gly Phe Gly Pro Asn Ser Asp Lys Leu Arg Tyr Gly Ser Leu Pro Arg 165	170	175	528	
gaa gct gtt tgt act gag aac ttg acc cca tgg cta aag tta ctt cct Glu Ala Val Cys Thr Glu Asn Leu Thr Pro Trp Leu Lys Leu Leu Pro 180	185	190	576	
tgt aga gat aag gat ggt att tct gcg tta atg aat agg cca tct gtt Cys Arg Asp Lys Asp Gly Ile Ser Ala Leu Met Asn Arg Pro Ser Val 195	200	205	624	
tac aga ggg ttt tat cat tct cag aga ttg cat tta tcc acg gtt gaa Tyr Arg Gly Phe Tyr His Ser Gln Arg Leu His Leu Ser Thr Val Glu 210	215	220	672	
tct ggt caa gag gga ttg ggt tct ggt ata gtg ctg gag cag acg ctt Ser Gly Gln Glu Gly Leu Gly Ser Gly Ile Val Leu Glu Gln Thr Leu 225	230	235	240	720
act gtt gtt ctt cag cct gag act act tct gtt gaa tca aat atg cag Thr Val Val Leu Gln Pro Glu Thr Thr Ser Val Glu Ser Asn Met Gln 245	250	255	768	
cca agt tgg tcc ctc agc tcc ctc ttt ggg aga caa gtt gtt ggg aga Pro Ser Trp Ser Leu Ser Ser Leu Phe Gly Arg Gln Val Val Gly Arg 260	265	270	816	
tgt gtt ctt gca aag tca agt aat gtg tat ctt caa ttg gaa ggt ctt Cys Val Leu Ala Lys Ser Ser Asn Val Tyr Leu Gln Leu Glu Gly Leu 275	280	285	864	
ctt ggt tac gaa tca aaa aac gtg gat aca gaa ata gaa gca cac caa Leu Gly Tyr Glu Ser Lys Asn Val Asp Thr Glu Ile Glu Ala His Gln 290	295	300	912	
cta tgg aag aat gca gag ttt gaa ttg tct ctt aag cca gag agg gtt Leu Trp Lys Asn Ala Glu Phe Glu Leu Ser Leu Lys Pro Glu Arg Val 305	310	315	320	960
att cga gaa agc tgc agc ttt ctt ttt att ttt gat att gac aaa tca Ile Arg Glu Ser Cys Ser Phe Leu Phe Ile Phe Asp Ile Asp Lys Ser 325	330	335	1008	
agt gac agc gag cca ttt gat ctt ggc ctt act tgg aag cgt ccc tca Ser Asp Ser Glu Pro Phe Asp Leu Gly Leu Thr Trp Lys Arg Pro Ser 340	345	350	1056	
aag tgg tca tgt caa caa gct cca tta cac tcg agt cgg ttt ttg atg Lys Trp Ser Cys Gln Gln Ala Pro Leu His Ser Ser Arg Phe Leu Met 355	360	365	1104	
gga agc ggg aac gaa aga ggt gca ata gcc atc ttg tta aaa gcg aca Gly Ser Gly Asn Glu Arg Gly Ala Ile Ala Ile Leu Leu Lys Ala Thr 370	375	380	1152	
gaa tct cag gag aag tta tca ggc aga gat ctc act aat ggc caa tgt Glu Ser Gln Glu Lys Leu Ser Gly Arg Asp Leu Thr Asn Gly Gln Cys 385	390	395	400	1200

aca ata aaa gca aat atc ttc cag att ttc cca tgg tat att aag gtt	1248		
Thr Ile Lys Ala Asn Ile Phe Gln Ile Phe Pro Trp Tyr Ile Lys Val			
405	410	415	
tat tat cat act cta caa atc ttt gtg gat caa caa cag aag aca gac	1296		
Tyr Tyr His Thr Leu Gln Ile Phe Val Asp Gln Gln Lys Thr Asp			
420	425	430	
agt gag gtc tta aag aag atc aat gtc tca cca tct acg gat aag gtg	1344		
Ser Glu Val Leu Lys Lys Ile Asn Val Ser Pro Ser Thr Asp Lys Val			
435	440	445	
tca tct ggc atg atg gag atg atg ttg gaa cta cca tgt gaa gtg aaa	1392		
Ser Ser Gly Met Met Glu Met Met Leu Glu Leu Pro Cys Glu Val Lys			
450	455	460	
tct gta gcc ata tca att gaa tat gat aag ggt ttt ctg cat ata gat	1440		
Ser Val Ala Ile Ser Ile Glu Tyr Asp Lys Gly Phe Leu His Ile Asp			
465	470	475	480
gaa tat cct cct gat gct aat caa gga ttc gac att cca tcg gct ttg	1488		
Glu Tyr Pro Pro Asp Ala Asn Gln Gly Phe Asp Ile Pro Ser Ala Leu			
485	490	495	
ata agc ttc ccc gat cat cat gct agt tta gat ttc caa gaa gag ctc	1536		
Ile Ser Phe Pro Asp His His Ala Ser Leu Asp Phe Gln Glu Glu Leu			
500	505	510	
agc aac tcg ccc tta tta tca agt tta aag gaa aaa tcc tta gta cgc	1584		
Ser Asn Ser Pro Leu Leu Ser Ser Leu Lys Glu Lys Ser Leu Val Arg			
515	520	525	
tct tac aca gaa gta ttg ctc gta cct ttg aca acc cct gat ttt agc	1632		
Ser Tyr Thr Glu Val Leu Leu Val Pro Leu Thr Thr Pro Asp Phe Ser			
530	535	540	
atg cct tac aac gta atc acg atc aca tgc acc atc ttc gca ttg tat	1680		
Met Pro Tyr Asn Val Ile Thr Ile Cys Thr Ile Phe Ala Leu Tyr			
545	550	555	560
ttt gga tca ttg cta aat gtt cta cgt aga cga att ggt gaa gaa gaa	1728		
Phe Gly Ser Leu Leu Asn Val Leu Arg Arg Arg Ile Gly Glu Glu			
565	570	575	
agg ttt ctc aaa agc caa gca gga aag aaa aca ggt ggg ctt aag cag	1776		
Arg Phe Leu Lys Ser Gln Ala Gly Lys Lys Thr Gly Gly Leu Lys Gln			
580	585	590	
tta tta tcg aga atc aca gcc aag att aga ggg aga cca att gaa gca	1824		
Leu Leu Ser Arg Ile Thr Ala Lys Ile Arg Gly Arg Pro Ile Glu Ala			
595	600	605	
cca tca tca tca gaa gct gaa tct tcg gtc ttg tct agt aaa ctt atc	1872		
Pro Ser Ser Ser Glu Ala Glu Ser Ser Val Leu Ser Ser Lys Leu Ile			
610	615	620	
tta aaa atc ata tta gtt gca gga gct gct gca gcg tgg caa tat ttt	1920		
Leu Lys Ile Ile Leu Val Ala Gly Ala Ala Ala Ala Trp Gln Tyr Phe			
625	630	635	640

tcc acg gac gag tag
Ser Thr Asp Glu

1935

<210> 68

<211> 644

<212> PRT

<213> *Arabidopsis thaliana*

<400> 68

Met Ala Ser Leu Leu Arg Ser Leu Ile Leu Leu Ile Val Gln Ser
1 5 10 15

Phe Leu Val Ala Ile Ala Phe Gly Ser Lys Glu Val Glu Glu Phe Ser
20 25 30

Glu Ala Leu Leu Leu Lys Pro Leu Pro Asp Arg Lys Val Leu Ala His
35 40 45

Phe His Phe Glu Asn Arg Ala Pro Pro Ser Asn Ser His Gly Arg His
50 55 60

His His Leu Phe Pro Lys Ala Ile Ser Gln Leu Val Gln Lys Phe Arg
65 70 75 80

Val Lys Glu Met Glu Leu Ser Phe Thr Gln Gly Arg Trp Asn His Glu
85 90 95

His Trp Gly Gly Phe Asp Pro Leu Ser Ser Met Asn Ala Lys Pro Val
100 105 110

Gly Val Glu Leu Trp Ala Val Phe Asp Val Pro Gln Ser Gln Val Asp
115 120 125

Thr Ser Trp Lys Asn Leu Thr His Ala Leu Ser Gly Leu Phe Cys Ala
130 135 140

Ser Ile Asn Phe Leu Glu Ser Ser Thr Ser Tyr Ala Ala Pro Thr Trp
145 150 155 160

Gly Phe Gly Pro Asn Ser Asp Lys Leu Arg Tyr Gly Ser Leu Pro Arg
165 170 175

Glu Ala Val Cys Thr Glu Asn Leu Thr Pro Trp Leu Lys Leu Leu Pro
180 185 190

Cys Arg Asp Lys Asp Gly Ile Ser Ala Leu Met Asn Arg Pro Ser Val
195 200 205

Tyr Arg Gly Phe Tyr His Ser Gln Arg Leu His Leu Ser Thr Val Glu
210 215 220

Ser Gly Gln Glu Gly Leu Gly Ser Gly Ile Val Leu Glu Gln Thr Leu
225 230 235 240

Thr Val Val Leu Gln Pro Glu Thr Thr Ser Val Glu Ser Asn Met Gln
245 250 255

Pro Ser Trp Ser Leu Ser Ser Leu Phe Gly Arg Gln Val Val Gly Arg
260 265 270

Cys Val Leu Ala Lys Ser Ser Asn Val Tyr Leu Gln Leu Glu Gly Leu
275 280 285

Leu Gly Tyr Glu Ser Lys Asn Val Asp Thr Glu Ile Glu Ala His Gln
290 295 300

Leu Trp Lys Asn Ala Glu Phe Glu Leu Ser Leu Lys Pro Glu Arg Val
305 310 315 320

Ile Arg Glu Ser Cys Ser Phe Leu Phe Ile Phe Asp Ile Asp Lys Ser
325 330 335

Ser Asp Ser Glu Pro Phe Asp Leu Gly Leu Thr Trp Lys Arg Pro Ser
340 345 350

Lys Trp Ser Cys Gln Gln Ala Pro Leu His Ser Ser Arg Phe Leu Met
355 360 365

Gly Ser Gly Asn Glu Arg Gly Ala Ile Ala Ile Leu Leu Lys Ala Thr
370 375 380

Glu Ser Gln Glu Lys Leu Ser Gly Arg Asp Leu Thr Asn Gly Gln Cys
385 390 395 400

Thr Ile Lys Ala Asn Ile Phe Gln Ile Phe Pro Trp Tyr Ile Lys Val
405 410 415

Tyr Tyr His Thr Leu Gln Ile Phe Val Asp Gln Gln Gln Lys Thr Asp
420 425 430

Ser Glu Val Leu Lys Lys Ile Asn Val Ser Pro Ser Thr Asp Lys Val
435 440 445

Ser Ser Gly Met Met Glu Met Met Leu Glu Leu Pro Cys Glu Val Lys
450 455 460

Ser Val Ala Ile Ser Ile Glu Tyr Asp Lys Gly Phe Leu His Ile Asp
465 470 475 480

Glu Tyr Pro Pro Asp Ala Asn Gln Gly Phe Asp Ile Pro Ser Ala Leu
485 490 495

Ile Ser Phe Pro Asp His His Ala Ser Leu Asp Phe Gln Glu Glu Leu
500 505 510

Ser Asn Ser Pro Leu Leu Ser Ser Leu Lys Glu Lys Ser Leu Val Arg
515 520 525

Ser Tyr Thr Glu Val Leu Leu Val Pro Leu Thr Thr Pro Asp Phe Ser
530 535 540

Met Pro Tyr Asn Val Ile Thr Ile Thr Cys Thr Ile Phe Ala Leu Tyr
545 550 555 560

Phe Gly Ser Leu Leu Asn Val Leu Arg Arg Arg Ile Gly Glu Glu Glu
565 570 575

Arg Phe Leu Lys Ser Gln Ala Gly Lys Lys Thr Gly Gly Leu Lys Gln
580 585 590

Leu Leu Ser Arg Ile Thr Ala Lys Ile Arg Gly Arg Pro Ile Glu Ala
595 600 605

Pro Ser Ser Ser Glu Ala Glu Ser Ser Val Leu Ser Ser Lys Leu Ile
610 615 620

Leu Lys Ile Ile Leu Val Ala Gly Ala Ala Ala Ala Trp Gln Tyr Phe
625 630 635 640

Ser Thr Asp Glu

<210> 69
 <211> 210
 <212> DNA
 <213> *Arabidopsis thaliana*

<220>
 <221> CDS
 <222> (1)..(210)
 <223> 47050A

<400> 69
 atg ggt gga gga gga cat ggc gga ggt ata act tac aag gga gtc act 48
 Met Gly Gly Gly His Gly Gly Ile Thr Tyr Lys Gly Val Thr
 1 5 10 15
 gtc cac act ccc aag act tgg cac acc gtc acc gga aaa ggc ttg tgc 96
 Val His Thr Pro Lys Thr Trp His Thr Val Thr Gly Lys Gly Leu Cys
 20 25 30
 gcc gtt atg tgg ttc tgg att ctg tac agg gca aag caa gat ggt cct 144
 Ala Val Met Trp Phe Trp Ile Leu Tyr Arg Ala Lys Gln Asp Gly Pro
 35 40 45
 gta gtt atg gga tgg agg cac cct tgg gat ggt cat ggt gat cac ggt 192
 Val Val Met Gly Trp Arg His Pro Trp Asp Gly His Gly Asp His Gly
 50 55 60
 cac gga gat cat cac tag 210
 His Gly Asp His His
 65

<210> 70
 <211> 69
 <212> PRT
 <213> *Arabidopsis thaliana*

<400> 70
 Met Gly Gly Gly His Gly Gly Ile Thr Tyr Lys Gly Val Thr 85
 1 5 10 15

Val His Thr Pro Lys Thr Trp His Thr Val Thr Gly Lys Gly Leu Cys
 20 25 30

Ala Val Met Trp Phe Trp Ile Leu Tyr Arg Ala Lys Gln Asp Gly Pro
 35 40 45

Val Val Met Gly Trp Arg His Pro Trp Asp Gly His Gly Asp His Gly
 50 55 60

His Gly Asp His His
 65

<210> 71

<211> 978

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (1)..(978)

<223> 52949A

<400> 71
 atg gct tct tct tct tgt ttc ctt cgc tcg att ctc ttc tct tct cct 48
 Met Ala Ser Ser Ser Cys Phe Leu Arg Ser Ile Leu Phe Ser Ser Pro
 1 5 10 15

act aac ctt cgt tca aat cac cat ctc ccc act ttc ttc ccc aag aat 96
 Thr Asn Leu Arg Ser Asn His His Leu Pro Thr Phe Phe Pro Lys Asn
 20 25 30

tat ctc att tgc tct cat tcc act tct tct cgc ttc gaa tcg ctc tcg 144
 Tyr Leu Ile Cys Ser His Ser Thr Ser Arg Phe Glu Ser Leu Ser
 35 40 45

gtt tca tcg atc gga act gga tct acc aag aaa tca tcc gat act cgg 192
 Val Ser Ser Ile Gly Thr Gly Ser Thr Lys Lys Ser Ser Asp Thr Arg
 50 55 60

aga aag gta aag agc atg gct acg aca aat ata gga aag gag gag aag 240
 Arg Lys Val Lys Ser Met Ala Thr Thr Asn Ile Gly Lys Glu Glu Lys
 65 70 75 80

aaa aga gtc gag att tat gat ctc gaa gag aat tta gtg att gat ttg 288
 Lys Arg Val Glu Ile Tyr Asp Leu Glu Glu Asn Leu Val Ile Asp Leu
 85 90 95

gct aaa ttc aca gca gat ctc tcc gat aag ttt tgt aaa gag aga ggc	100	105	110	336
Ala Lys Phe Thr Ala Asp Leu Ser Asp Lys Phe Cys Lys Glu Arg Gly				
gct ttc acc gtc gtt gtc tcc ggt ggc tct ctc atc aaa tca ctc cgg	115	120	125	384
Ala Phe Thr Val Val Ser Gly Gly Ser Leu Ile Lys Ser Leu Arg				
aaa tta gta gaa tct cct tac gtt gat tct ata gat tgg gca agg tgg	130	135	140	432
Lys Leu Val Glu Ser Pro Tyr Val Asp Ser Ile Asp Trp Ala Arg Trp				
cat ttt ttc tgg gtt gac gag aga gtt gtt ccc aag aat cac gat gat	145	150	155	480
His Phe Phe Trp Val Asp Glu Arg Val Val Pro Lys Asn His Asp Asp				
agc aac tat aaa ctc gct tat gat agt ttt cta tcc aag gta cca att	165	170	175	528
Ser Asn Tyr Lys Leu Ala Tyr Asp Ser Phe Leu Ser Lys Val Pro Ile				
ccg cct gga aat gta tat gca atc aac gaa gcc ctc tcc gct gag gct	180	185	190	576
Pro Pro Gly Asn Val Tyr Ala Ile Asn Glu Ala Leu Ser Ala Glu Ala				
gca gcg gat gat tac gag acc tgc ctc aaa cat ttg gtc aac acc aac	195	200	205	624
Ala Ala Asp Asp Tyr Glu Thr Cys Leu Lys His Leu Val Asn Thr Asn				
att ctc cgt gta tct gaa tca act ggc ttt ccc aaa ttt gat ctc atg	210	215	220	672
Ile Leu Arg Val Ser Glu Ser Thr Gly Phe Pro Lys Phe Asp Leu Met				
ctt cta ggt atg gga cct gat ggt cat gtg gca tca tta ttc cct ggg	225	230	235	720
Leu Leu Gly Met Gly Pro Asp Gly His Val Ala Ser Leu Phe Pro Gly				
cat ggt ctc tgc aac gag agc aag aaa tgg gta gtt tca atc tct gac	245	250	255	768
His Gly Leu Cys Asn Glu Ser Lys Lys Trp Val Val Ser Ile Ser Asp				
tct cca aaa cca ccg tct gag aga atc acc ttc acg ttc ccg gtc atc	260	265	270	816
Ser Pro Lys Pro Ser Glu Arg Ile Thr Phe Thr Phe Pro Val Ile				
aac tca tct gca cat gta gct cta gtt gtt tgc ggt tct ggg aaa gct	275	280	285	864
Asn Ser Ser Ala His Val Ala Leu Val Val Cys Gly Ser Gly Lys Ala				
gaa gct gtg gag gca gct tta aag aag act ggg aat gta cca cct gct	290	295	300	912
Glu Ala Val Glu Ala Ala Leu Lys Lys Thr Gly Asn Val Pro Pro Ala				
ggt tct gtt tct gct gaa gac gag ttg gtt tgg ttc ctg gac aaa cca	305	310	315	960
Gly Ser Val Ser Ala Glu Asp Glu Leu Val Trp Phe Leu Asp Lys Pro				
gca tct tcc aag ctc taa	325			978
Ala Ser Ser Lys Leu				

<210> 72

<211> 325

<212> PRT

<213> *Arabidopsis thaliana*

<400> 72

Met Ala Ser Ser Ser Cys Phe Leu Arg Ser Ile Leu Phe Ser Ser Pro
1 5 10 15

Thr Asn Leu Arg Ser Asn His His Leu Pro Thr Phe Phe Pro Lys Asn
20 25 30

Tyr Leu Ile Cys Ser His Ser Thr Ser Ser Arg Phe Glu Ser Leu Ser
35 40 45

Val Ser Ser Ile Gly Thr Gly Ser Thr Lys Lys Ser Ser Asp Thr Arg
50 55 60

Arg Lys Val Lys Ser Met Ala Thr Thr Asn Ile Gly Lys Glu Glu Lys
65 70 75 80

Lys Arg Val Glu Ile Tyr Asp Leu Glu Glu Asn Leu Val Ile Asp Leu
85 90 95

Ala Lys Phe Thr Ala Asp Leu Ser Asp Lys Phe Cys Lys Glu Arg Gly
100 105 110

Ala Phe Thr Val Val Val Ser Gly Gly Ser Leu Ile Lys Ser Leu Arg
115 120 125

Lys Leu Val Glu Ser Pro Tyr Val Asp Ser Ile Asp Trp Ala Arg Trp
130 135 140

His Phe Phe Trp Val Asp Glu Arg Val Val Pro Lys Asn His Asp Asp
145 150 155 160

Ser Asn Tyr Lys Leu Ala Tyr Asp Ser Phe Leu Ser Lys Val Pro Ile
165 170 175

Pro Pro Gly Asn Val Tyr Ala Ile Asn Glu Ala Leu Ser Ala Glu Ala
180 185 190

Ala Ala Asp Asp Tyr Glu Thr Cys Leu Lys His Leu Val Asn Thr Asn
195 200 205

Ile Leu Arg Val Ser Glu Ser Thr Gly Phe Pro Lys Phe Asp Leu Met
210 215 220

Leu Leu Gly Met Gly Pro Asp Gly His Val Ala Ser Leu Phe Pro Gly
225 230 235 240

His Gly Leu Cys Asn Glu Ser Lys Lys Trp Val Val Ser Ile Ser Asp
245 250 255

Ser Pro Lys Pro Pro Ser Glu Arg Ile Thr Phe Thr Phe Pro Val Ile
260 265 270

Asn Ser Ser Ala His Val Ala Leu Val Val Cys Gly Ser Gly Lys Ala
275 280 285

Glu Ala Val Glu Ala Ala Leu Lys Lys Thr Gly Asn Val Pro Pro Ala
290 295 300

Gly Ser Val Ser Ala Glu Asp Glu Leu Val Trp Phe Leu Asp Lys Pro
305 310 315 320

Ala Ser Ser Lys Leu
325

<210> 73

<211> 2343

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (1)..(2343)

<223> 53210A

<400> 73

atg gct cct gct ttg agt aga agt ctc tac aca tct cct ttg act tca

48

Met Ala Pro Ala Leu Ser Arg Ser Leu Tyr Thr Ser Pro Leu Thr Ser		
1 5 10 15		
gtt cca atc act cct gtc tct cgt ctc tct cat ctg aga agc tcg		96
Val Pro Ile Thr Pro Val Ser Ser Arg Leu Ser His Leu Arg Ser Ser		
20 25 30		
ttt ctc cca cac ggc ggc gct tta aga acc ggc gtt tcg tgt agc tgg		144
Phe Leu Pro His Gly Gly Ala Leu Arg Thr Gly Val Ser Cys Ser Trp		
35 40 45		
aat ctc gaa aag aga tgt aac cga ttc gcc gtg aag tgt gac gcc gcc		192
Asn Leu Glu Lys Arg Cys Asn Arg Phe Ala Val Lys Cys Asp Ala Ala		
50 55 60		
gtg gcg gag aaa gag acc act gaa gaa ggg tca ggt gag aag ttt gag		240
Val Ala Glu Lys Glu Thr Thr Glu Glu Gly Ser Gly Glu Lys Phe Glu		
65 70 75 80		
tac caa gct gag gtt agt aga ttg ttg gat ttg att gtt cat agc tta		288
Tyr Gln Ala Glu Val Ser Arg Leu Leu Asp Leu Ile Val His Ser Leu		
85 90 95		
tac agt cac aag gag gtg ttt ctc agg gag ctt gta agt aat gca agt		336
Tyr Ser His Lys Glu Val Phe Leu Arg Glu Leu Val Ser Asn Ala Ser		
100 105 110		
gat gct ttg gat aag ctg agg ttc ttg agt gta aca gag cct tct ttg		384
Asp Ala Leu Asp Lys Leu Arg Phe Leu Ser Val Thr Glu Pro Ser Leu		
115 120 125		
ctt gga gat ggt gga gat ctt gag att agg att aag cct gat cct gat		432
Leu Gly Asp Gly Asp Leu Glu Ile Arg Ile Lys Pro Asp Pro Asp		
130 135 140		
aac ggc acc atc acc ata act gat act ggt att gga atg aca aag gaa		480
Asn Gly Thr Ile Thr Ile Asp Thr Gly Ile Gly Met Thr Lys Glu		
145 150 155 160		
gaa ctt att gat tgc ctt gga act att gct caa agt ggt act tcg aaa		528
Glu Leu Ile Asp Cys Leu Gly Thr Ile Ala Gln Ser Gly Thr Ser Lys		
165 170 175		
ttc ttg aag gct cta aag gaa aac aag gac ctt ggt gct gac aac ggt		576
Phe Leu Lys Ala Leu Lys Glu Asn Lys Asp Leu Gly Ala Asp Asn Gly		
180 185 190		
ttg atc gga cag ttt ggt gtt ggg ttt tac tct gct ttc tta gtt gct		624
Leu Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Leu Val Ala		
195 200 205		
gag aag gtt gtt gtg tcc acc aaa agc ccc aaa tct gac aag caa tat		672
Glu Lys Val Val Val Ser Thr Lys Ser Pro Lys Ser Asp Lys Gln Tyr		
210 215 220		
gtt tgg gaa tcg gtt gcc gat agt agc tcg tat ctg atc aga gaa gaa		720
Val Trp Glu Ser Val Ala Asp Ser Ser Ser Tyr Leu Ile Arg Glu Glu		
225 230 235 240		
aca gac cct gat aac att cta cgt cgt gga aca caa atc acc ttg tat		768

Thr Asp Pro Asp Asn Ile Leu Arg Arg Gly Thr Gln Ile Thr Leu Tyr			
245	250	255	
ctg agg gag gat gat aaa tac gaa ttt gcg gag tct aca agg atc aag			816
Leu Arg Glu Asp Asp Lys Tyr Glu Phe Ala Glu Ser Thr Arg Ile Lys			
260	265	270	
aac ctc gtg aag aat tac tct cag ttc gtt ggg ttt cct atc tat aca			864
Asn Leu Val Lys Asn Tyr Ser Gln Phe Val Gly Phe Pro Ile Tyr Thr			
275	280	285	
tgg cag gag aaa tca agg act ata gag gtc gaa gag gac gaa cca gtt			912
Trp Gln Glu Lys Ser Arg Thr Ile Glu Val Glu Asp Glu Pro Val			
290	295	300	
aag gaa gga gaa gag ggt gag cca aag aaa aag aag acc act aaa act			960
Lys Glu Gly Glu Gly Glu Pro Lys Lys Lys Thr Thr Lys Thr			
305	310	315	320
gag aag tat tgg gat tgg gaa cta gcc aac gag acc aaa ccg cta tgg			1008
Glu Lys Tyr Trp Asp Trp Glu Leu Ala Asn Glu Thr Lys Pro Leu Trp			
325	330	335	
atg cgc aat tcg aag gaa gtg gaa aaa gga gag tac aat gag ttc tac			1056
Met Arg Asn Ser Lys Glu Val Glu Lys Gly Glu Tyr Asn Glu Phe Tyr			
340	345	350	
aaa aag gct ttc aat gag ttc ttg gat cca ctt gct cac aca cac ttc			1104
Lys Lys Ala Phe Asn Glu Phe Leu Asp Pro Leu Ala His Thr His Phe			
355	360	365	
aca act gag ggt gag gtt gag ttc agg agc att ttg tac atc cct ggg			1152
Thr Thr Glu Gly Glu Val Glu Phe Arg Ser Ile Leu Tyr Ile Pro Gly			
370	375	380	
atg ggt cct ctt aac aat gaa gat gtt aca aac ccg aaa aca aag aac			1200
Met Gly Pro Leu Asn Asn Glu Asp Val Thr Asn Pro Lys Thr Lys Asn			
385	390	395	400
att cgt ctc tac gtg aag cgt gtg ttt atc tct gac gat ttt gat gga			1248
Ile Arg Leu Tyr Val Lys Arg Val Phe Ile Ser Asp Asp Phe Asp Gly			
405	410	415	
gag ctt ttc ccg aga tat ctg agc ttt gtg aag gga gtt gtg gac tct			1296
Glu Leu Phe Pro Arg Tyr Ile Ser Phe Val Lys Gly Val Val Asp Ser			
420	425	430	
gat gat ctt cct ctt aat gtt tct cgt gaa att ctc caa gaa agc aga			1344
Asp Asp Leu Pro Leu Asn Val Ser Arg Glu Ile Leu Gln Glu Ser Arg			
435	440	445	
att gta aga atc atg aga aag agg ctc att aga aaa acc ttt gac atg			1392
Ile Val Arg Ile Met Arg Lys Arg Leu Ile Arg Lys Thr Phe Asp Met			
450	455	460	
ata caa gaa atc tct gag agt gaa aac aaa gag gat tac aag aaa ttc			1440
Ile Gln Glu Ile Ser Glu Ser Glu Asn Lys Glu Asp Tyr Lys Lys Phe			
465	470	475	480
tgg gag aac ttt ggt aga ttc ctt aaa ttg ggt tgt att gaa gac acc			1488

Trp Glu Asn Phe Gly Arg Phe Leu Lys Leu Gly Cys Ile Glu Asp Thr		
485	490	495
ggt aac cac aag cgt atc aca ccg cta ctt aga ttc ttc agt tcc aag		1536
Gly Asn His Lys Arg Ile Thr Pro Leu Leu Arg Phe Phe Ser Ser Lys		
500	505	510
aat gaa gag gaa ttg aca agc ttg gat gat tat atc gag aac atg gga		1584
Asn Glu Glu Leu Thr Ser Leu Asp Asp Tyr Ile Glu Asn Met Gly		
515	520	525
gag aac caa aag gcg atc tac tac ctc gca act gat agt ctt aaa agt		1632
Glu Asn Gln Lys Ala Ile Tyr Tyr Leu Ala Thr Asp Ser Leu Lys Ser		
530	535	540
gcc aag tct gcc cct ttc ttg gag aaa cta atc caa aaa gat atc gag		1680
Ala Lys Ser Ala Pro Phe Leu Glu Lys Leu Ile Gln Lys Asp Ile Glu		
545	550	555
560		
gtt cta tat ttg gtt gaa cca atc gat gaa gtt gct att cag aat ttg		1728
Val Leu Tyr Leu Val Glu Pro Ile Asp Glu Val Ala Ile Gln Asn Leu		
565	570	575
caa acc tac aaa gaa aag aaa ttc gtt gat atc agt aaa gaa gat ttg		1776
Gln Thr Tyr Lys Glu Lys Lys Phe Val Asp Ile Ser Lys Glu Asp Leu		
580	585	590
gaa ctc gga gat gaa gat gaa gta aag gac agg gaa gcg aaa caa gag		1824
Glu Leu Gly Asp Glu Asp Glu Val Lys Asp Arg Glu Ala Lys Gln Glu		
595	600	605
ttt aac ctt ctc tgt gac tgg ata aaa cag cag ctc ggt gac aaa gtt		1872
Phe Asn Leu Leu Cys Asp Trp Ile Lys Gln Gln Leu Gly Asp Lys Val		
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Ala Lys Val Gln Val Ser Asn Arg Leu Ser Ser Pro Cys Val Leu		
625	630	635
640		
gtc tct ggc aaa ttc ggg tgg tca gct aat atg gaa agg cta atg aag		1968
Val Ser Gly Lys Phe Gly Trp Ser Ala Asn Met Glu Arg Leu Met Lys		
645	650	655
gca cag gct ctt gga gac act tca agc ctg gag ttc atg aga ggt agg		2016
Ala Gln Ala Leu Gly Asp Thr Ser Ser Leu Glu Phe Met Arg Gly Arg		
660	665	670
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Arg Ile Leu Glu Ile Asn Pro Asp His Pro Ile Ile Lys Asp Leu Asn		
675	680	685
gct gct tgt aag aat gca cca gag agc act gaa gca aca aga gtg gtc		2112
Ala Ala Cys Lys Asn Ala Pro Glu Ser Thr Glu Ala Thr Arg Val Val		
690	695	700
gat ctc ttg tat gac act gct ata ata tca agt gga ttc act cct gat		2160
Asp Leu Leu Tyr Asp Thr Ala Ile Ile Ser Ser Gly Phe Thr Pro Asp		
705	710	715
720		
agc ccg gcc gag ctc ggg aac aag ata tat gag atg atg gca atg gcg		2208

Ser Pro Ala Glu Leu Gly Asn Lys Ile Tyr Glu Met Met Ala Met Ala			
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Val Gly Gly Arg Trp Gly Arg Val Glu Glu Glu Glu Ser Ser Thr			
740	745	750	
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Val Asn Glu Gly Asp Asp Lys Ser Gly Glu Thr Glu Val Val Glu Pro			
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Phe Leu Pro His Gly Gly Ala Leu Arg Thr Gly Val Ser Cys Ser Trp			
35	40	45	
Asn Leu Glu Lys Arg Cys Asn Arg Phe Ala Val Lys Cys Asp Ala Ala			
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Val Ala Glu Lys Glu Thr Thr Glu Glu Gly Ser Gly Glu Lys Phe Glu			
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Tyr Gln Ala Glu Val Ser Arg Leu Leu Asp Leu Ile Val His Ser Leu			
85	90	95	
Tyr Ser His Lys Glu Val Phe Leu Arg Glu Leu Val Ser Asn Ala Ser			
100	105	110	
Asp Ala Leu Asp Lys Leu Arg Phe Leu Ser Val Thr Glu Pro Ser Leu			
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Leu Gly Asp Gly Gly Asp Leu Glu Ile Arg Ile Lys Pro Asp Pro Asp
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Asn Gly Thr Ile Thr Ile Thr Asp Thr Gly Ile Gly Met Thr Lys Glu
145 150 155 160

Glu Leu Ile Asp Cys Leu Gly Thr Ile Ala Gln Ser Gly Thr Ser Lys
165 170 175

Phe Leu Lys Ala Leu Lys Glu Asn Lys Asp Leu Gly Ala Asp Asn Gly
180 185 190

Leu Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Leu Val Ala
195 200 205

Glu Lys Val Val Val Ser Thr Lys Ser Pro Lys Ser Asp Lys Gln Tyr
210 215 220

Val Trp Glu Ser Val Ala Asp Ser Ser Ser Tyr Leu Ile Arg Glu Glu
225 230 235 240

Thr Asp Pro Asp Asn Ile Leu Arg Arg Gly Thr Gln Ile Thr Leu Tyr
245 250 255

Leu Arg Glu Asp Asp Lys Tyr Glu Phe Ala Glu Ser Thr Arg Ile Lys
260 265 270

Asn Leu Val Lys Asn Tyr Ser Gln Phe Val Gly Phe Pro Ile Tyr Thr
275 280 285

Trp Gln Glu Lys Ser Arg Thr Ile Glu Val Glu Asp Glu Pro Val
290 295 300

Lys Glu Gly Glu Glu Gly Glu Pro Lys Lys Lys Lys Thr Thr Lys Thr
305 310 315 320

Glu Lys Tyr Trp Asp Trp Glu Leu Ala Asn Glu Thr Lys Pro Leu Trp
325 330 335

Met Arg Asn Ser Lys Glu Val Glu Lys Gly Glu Tyr Asn Glu Phe Tyr
340 345 350

Lys Lys Ala Phe Asn Glu Phe Leu Asp Pro Leu Ala His Thr His Phe
355 360 365

Thr Thr Glu Gly Glu Val Glu Phe Arg Ser Ile Leu Tyr Ile Pro Gly
370 375 380

Met Gly Pro Leu Asn Asn Glu Asp Val Thr Asn Pro Lys Thr Lys Asn
385 390 395 400

Ile Arg Leu Tyr Val Lys Arg Val Phe Ile Ser Asp Asp Phe Asp Gly
405 410 415

Glu Leu Phe Pro Arg Tyr Leu Ser Phe Val Lys Gly Val Val Asp Ser
420 425 430

Asp Asp Leu Pro Leu Asn Val Ser Arg Glu Ile Leu Gln Glu Ser Arg
435 440 445

Ile Val Arg Ile Met Arg Lys Arg Leu Ile Arg Lys Thr Phe Asp Met
450 455 460

Ile Gln Glu Ile Ser Glu Ser Glu Asn Lys Glu Asp Tyr Lys Lys Phe
465 470 475 480

Trp Glu Asn Phe Gly Arg Phe Leu Lys Leu Gly Cys Ile Glu Asp Thr
485 490 495

Gly Asn His Lys Arg Ile Thr Pro Leu Leu Arg Phe Phe Ser Ser Lys
500 505 510

Asn Glu Glu Glu Leu Thr Ser Leu Asp Asp Tyr Ile Glu Asn Met Gly
515 520 525

Glu Asn Gln Lys Ala Ile Tyr Tyr Leu Ala Thr Asp Ser Leu Lys Ser
530 535 540

Ala Lys Ser Ala Pro Phe Leu Glu Lys Leu Ile Gln Lys Asp Ile Glu
545 550 555 560

Val Leu Tyr Leu Val Glu Pro Ile Asp Glu Val Ala Ile Gln Asn Leu
565 570 575

Gln Thr Tyr Lys Glu Lys Lys Phe Val Asp Ile Ser Lys Glu Asp Leu
580 585 590

Glu Leu Gly Asp Glu Asp Glu Val Lys Asp Arg Glu Ala Lys Gln Glu
595 600 605

Phe Asn Leu Leu Cys Asp Trp Ile Lys Gln Gln Leu Gly Asp Lys Val
610 615 620

Ala Lys Val Gln Val Ser Asn Arg Leu Ser Ser Ser Pro Cys Val Leu
625 630 635 640

Val Ser Gly Lys Phe Gly Trp Ser Ala Asn Met Glu Arg Leu Met Lys
645 650 655

Ala Gln Ala Leu Gly Asp Thr Ser Ser Leu Glu Phe Met Arg Gly Arg
660 665 670

Arg Ile Leu Glu Ile Asn Pro Asp His Pro Ile Ile Lys Asp Leu Asn
675 680 685

Ala Ala Cys Lys Asn Ala Pro Glu Ser Thr Glu Ala Thr Arg Val Val
690 695 700

Asp Leu Leu Tyr Asp Thr Ala Ile Ile Ser Ser Gly Phe Thr Pro Asp
705 710 715 720

Ser Pro Ala Glu Leu Gly Asn Lys Ile Tyr Glu Met Met Ala Met Ala
725 730 735

Val Gly Gly Arg Trp Gly Arg Val Glu Glu Glu Glu Ser Ser Thr
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 Pro Ser Glu Asn Val Leu Arg Phe Ser Val Ala Ser Arg Leu Phe Ser
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 cct aaa tgg aag aaa agt ttc att agt tta cct tgt cgt agt aaa act 144
 Pro Lys Trp Lys Lys Ser Phe Ile Ser Leu Pro Cys Arg Ser Lys Thr
 35 40 45

 acg agg aag gtt ttg gcg tca agc cgt tat gtg cca ggg aaa ttg gaa 192
 Thr Arg Lys Val Leu Ala Ser Ser Arg Tyr Val Pro Gly Lys Leu Glu
 50 55 60

 gat ttg tcg gtt gtt aag aag agt tta ccg aga aga gaa cct gtg gag 240
 Asp Leu Ser Val Val Lys Lys Ser Leu Pro Arg Arg Glu Pro Val Glu
 65 70 75 80

 aag ctt ggt ttt gtg agg act ttg ttg att gat aat tat gat agt tat 288
 Lys Leu Gly Phe Val Arg Thr Leu Leu Ile Asp Asn Tyr Asp Ser Tyr
 85 90 95

 aca ttc aat ata tat cag gct ctg agt act att aat gga gtg cct cct 336
 Thr Phe Asn Ile Tyr Gln Ala Leu Ser Thr Ile Asn Gly Val Pro Pro
 100 105 110

 gtc gtt att cgg aat gat gag tgg acg tgg gaa gaa gct tac cat tac 384
 Val Val Ile Arg Asn Asp Glu Trp Thr Trp Glu Glu Ala Tyr His Tyr
 115 120 125

 tta tat gaa gat gtt gct ttt gat aat att gtt ata tcg cct gga cct 432
 Leu Tyr Glu Asp Val Ala Phe Asp Asn Ile Val Ile Ser Pro Gly Pro
 130 135 140

 ggt tcg cct atg tgt cca gct gat ata gga ata tgt ctt cgt ctt ttg 480
 Gly Ser Pro Met Cys Pro Ala Asp Ile Gly Ile Cys Leu Arg Leu Leu
 145 150 155 160

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 165 170 175

 gca cta ggt tat gtc cat gga gct cat gtg gtg cat gcc ccg gaa cca 576
 Ala Leu Gly Tyr Val His Gly Ala His Val Val His Ala Pro Glu Pro
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 Val His Gly Arg Leu Ser Gly Ile Glu His Asp Gly Asn Ile Leu Phe
 195 200 205

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 210 215 220

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His Ser Leu Ile Ile Asp Lys Glu Ser Leu Pro Lys Glu Leu Val Pro	
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Ile Ala Trp Thr Ile Tyr Asp Asp Thr Gly Ser Phe Ser Glu Lys Asn	
245 250 255	
tcc tgt gtt cct gtg aat aac act ggg agc cca ctt ggg aac gga tct	816
Ser Cys Val Pro Val Asn Asn Thr Gly Ser Pro Leu Gly Asn Gly Ser	
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gtc att cct gtt tca gaa aag tta gaa aat cga agt cat tgg cct tcg	864
Val Ile Pro Val Ser Glu Lys Leu Glu Asn Arg Ser His Trp Pro Ser	
275 280 285	
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Ser His Val Asn Gly Lys Gln Asp Arg His Ile Leu Met Gly Ile Met	
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His Ser Ser Phe Pro His Tyr Gly Leu Gln Phe His Pro Glu Ser Ile	
305 310 315 320	
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Ala Thr Thr Tyr Gly Ser Gln Leu Phe Lys Asn Phe Lys Asp Ile Thr	
325 330 335	
gtg aat tat tgg agt cgg tgc aaa tct aca tcc ctg cgt cga aga aac	1056
Val Asn Tyr Trp Ser Arg Cys Lys Ser Thr Ser Leu Arg Arg Arg Asn	
340 345 350	
ata aat gac act gca aac atg cag gtg cct gat gct act caa ttg ctg	1104
Ile Asn Asp Thr Ala Asn Met Gln Val Pro Asp Ala Thr Gln Leu Leu	
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Arg Leu Lys Trp Lys Lys His Glu Arg Leu Ala His Lys Val Gly Gly	
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Lys Leu Gly Phe Val Arg Thr Leu Leu Ile Asp Asn Tyr Asp Ser Tyr
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Val Val Ile Arg Asn Asp Glu Trp Thr Trp Glu Glu Ala Tyr His Tyr
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Ser Asp Ile Pro Ser Gly Arg Asn Ser Asp Phe Lys Val Val Arg Tyr
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225 230 235 240

Ile Ala Trp Thr Ile Tyr Asp Asp Thr Gly Ser Phe Ser Glu Lys Asn
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Ser Cys Val Pro Val Asn Asn Thr Gly Ser Pro Leu Gly Asn Gly Ser
260 265 270

Val Ile Pro Val Ser Glu Lys Leu Glu Asn Arg Ser His Trp Pro Ser
275 280 285

Ser His Val Asn Gly Lys Gln Asp Arg His Ile Leu Met Gly Ile Met
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His Ser Ser Phe Pro His Tyr Gly Leu Gln Phe His Pro Glu Ser Ile
305 310 315 320

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580 585 590

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595 600 605

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Thr Leu Pro Val Ile Asp Ser Ser Gln Ser Lys Thr Ser Phe Val Pro
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Asp Lys Ser Arg Glu Gln Tyr Ile Asn Asp Val Gln Ser Cys Met Lys
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Tyr Ile Lys Asp Gly Glu Ser Tyr Glu Leu Cys Leu Thr Thr Gln Asn
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Arg Arg Lys Ile Gly Asn Ala Asp Pro Leu Gly Leu Tyr Leu His Leu
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Arg Glu Arg Asn Pro Ala Pro Tyr Ala Ala Phe Leu Asn Phe Ser Asn
690 695 700

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Asp Arg Asn Gly Met Leu Glu Ala Lys Pro Ile Lys Gly Thr Ile Ala
725 730 735

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740 745 750

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755 760 765

Arg Asn Asp Leu Gly Arg Val Cys Glu Pro Gly Ser Val His Val Pro
770 775 780

Asn Leu Met Asp Val Glu Ser Tyr Thr Thr Val His Thr Met Val Ser
785 790 795 800

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805 810 815

Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly Ala Pro Lys Leu Arg
820 825 830

Ser Val Glu Ile Leu Asp Ser Leu Glu Asn Cys Ser Arg Gly Leu Tyr
835 840 845

Ser Gly Ser Ile Gly Tyr Phe Ser Tyr Asn Gly Thr Phe Asp Leu Asn
850 855 860

Ile Val Ile Arg Thr Val Ile Ile His Glu Asp Glu Ala Ser Ile Gly
865 870 875 880

Ala Gly Gly Ala Ile Val Ala Leu Ser Ser Pro Glu Asp Glu Phe Glu
885 890 895

Glu Met Ile Leu Lys Thr Arg Ala Pro Ala Asn Ala Val Met Glu Phe
900 905 910

Cys Ser Asp Gln Arg Arg Gln
915

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 <223> 58351A

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1 5 10 15		
gaa gag aag cag atg aga ctc gcc gaa aac gta gcc ggt aca agg aaa		96
Glu Glu Lys Gln Met Arg Leu Ala Glu Asn Val Ala Gly Thr Arg Lys		
20 25 30		
gcc gcc act gag att ctt cag ctt tgt ttc gat gct aag gat tgg aaa		144
Ala Ala Thr Glu Ile Leu Gln Leu Cys Phe Asp Ala Lys Asp Trp Lys		
35 40 45		
ctt ctg aat gag cag att ctc aat ctc tct aag aaa cgt ggt cag ctc		192
Leu Leu Asn Glu Gln Ile Leu Asn Leu Ser Lys Lys Arg Gly Gln Leu		
50 55 60		
aaa cag gct gtg caa tcc atg gtg cag caa gca atg cag tat atc gat		240
Lys Gln Ala Val Gln Ser Met Val Gln Gln Ala Met Gln Tyr Ile Asp		
65 70 75 80		
cag aca cca gac att gaa act cgg ata gag ctt atc aag acg ctg aac		288
Gln Thr Pro Asp Ile Glu Thr Arg Ile Glu Leu Ile Lys Thr Leu Asn		
85 90 95		
aat gta tct gct gga aag ata tat gtt gaa atc gag agg gca cgt ctc		336
Asn Val Ser Ala Gly Lys Ile Tyr Val Glu Ile Glu Arg Ala Arg Leu		
100 105 110		
acc aag aaa ctt gct aag att aag gaa gaa cag ggt cag ata gct gaa		384
Thr Lys Lys Leu Ala Lys Ile Lys Glu Glu Gln Gly Gln Ile Ala Glu		
115 120 125		
gct gca gat ctt atg caa gaa gtt gct gtg gag aca ttt ggt gct atg		432
Ala Ala Asp Leu Met Gln Glu Val Ala Val Glu Thr Phe Gly Ala Met		
130 135 140		
gca aaa act gag aaa att gca ttt atc ctt gaa caa gtt cgc ttg tgc		480

Ala Lys Thr Glu Lys Ile Ala Phe Ile Leu Glu Gln Val Arg Leu Cys			
145	150	155	160
ttg gat cgt caa gat ttt gtt cgt gca caa atc tta tct agg aag atc			528
Leu Asp Arg Gln Asp Phe Val Arg Ala Gln Ile Leu Ser Arg Lys Ile			
165	170	175	
aat cct aga gtt ttt gac gca gat aca aaa aaa gat aag aag aaa cct			576
Asn Pro Arg Val Phe Asp Ala Asp Thr Lys Lys Asp Lys Lys Pro			
180	185	190	
aag gaa ggt gat aac atg gta gaa gag gct cct gct gat ata cca acc			624
Lys Glu Gly Asp Asn Met Val Glu Glu Ala Pro Ala Asp Ile Pro Thr			
195	200	205	
ctt ttg gag ctt aag cga att tac tac gag ctt atg att cgg tac tat			672
Leu Leu Glu Leu Lys Arg Ile Tyr Tyr Glu Leu Met Ile Arg Tyr Tyr			
210	215	220	
tct cat aac aat gag tac att gaa atc tgc cgt agc tac aag gcg ata			720
Ser His Asn Asn Glu Tyr Ile Glu Ile Cys Arg Ser Tyr Lys Ala Ile			
225	230	235	240
tat gat atc cct tca gta aaa gaa act ccg gag cag tgg att ccg gtc			768
Tyr Asp Ile Pro Ser Val Lys Glu Thr Pro Glu Gln Trp Ile Pro Val			
245	250	255	
ctg agg aag atc tgc tgg ttc ttg gtc ttg gca cct cat gac cca atg			816
Leu Arg Lys Ile Cys Trp Phe Leu Val Leu Ala Pro His Asp Pro Met			
260	265	270	
caa tca agc ttg ctc aat gca act ctg gaa gac aag aat tta tca gaa			864
Gln Ser Ser Leu Leu Asn Ala Thr Leu Glu Asp Lys Asn Leu Ser Glu			
275	280	285	
atc cct gat ttc aag atg ctt cta aaa cag gta gtg aca atg gag gtt			912
Ile Pro Asp Phe Lys Met Leu Leu Lys Gln Val Val Thr Met Glu Val			
290	295	300	
att caa tgg aca tct ctg tgg aac aaa tac aag gat gag ttc gag aaa			960
Ile Gln Trp Thr Ser Leu Trp Asn Lys Tyr Lys Asp Glu Phe Glu Lys			
305	310	315	320
gag aaa agc atg att gga ggt tct ttg ggt gac aaa gct ggt gaa gat			1008
Glu Lys Ser Met Ile Gly Gly Ser Leu Gly Asp Lys Ala Gly Glu Asp			
325	330	335	
ctg aaa ctg aga atc atc gaa cat aat atc ctc gtt gtc tca aag tac			1056
Leu Lys Leu Arg Ile Ile Glu His Asn Ile Leu Val Val Ser Lys Tyr			
340	345	350	
tac gca agg ata acc tta aag aga ctt gcc gag ctt tta tgc ctg agc			1104
Tyr Ala Arg Ile Thr Leu Lys Arg Leu Ala Glu Leu Leu Cys Leu Ser			
355	360	365	
atg gag gag ggc gag aag cat cta tcg gag atg gta gtg tca aaa gca			1152
Met Glu Glu Ala Glu Lys His Leu Ser Glu Met Val Val Ser Lys Ala			
370	375	380	
ctg att gca aaa ata gac aga cca tct gga att gtg tgc ttc cag atc			1200

Leu Ile Ala Lys Ile Asp Arg Pro Ser Gly Ile Val Cys Phe Gln Ile				
385	390	395	400	
gca aag gac agc aac gag att cta aac tcg tgg gca ggg aat ttg gag				1248
Ala Lys Asp Ser Asn Glu Ile Leu Asn Ser Trp Ala Gly Asn Leu Glu				
405	410	415		
aag ctt cta gat ctt gtg gaa aag agt tgc cac caa att cac aag gaa				1296
Lys Leu Leu Asp Leu Val Glu Lys Ser Cys His Gln Ile His Lys Glu				
420	425	430		
acc atg gtt cac aaa gcc gct ctc aga cct tga				1329
Thr Met Val His Lys Ala Ala Leu Arg Pro				
435	440			
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<213> <i>Arabidopsis thaliana</i>				
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Glu Glu Lys Gln Met Arg Leu Ala Glu Asn Val Ala Gly Thr Arg Lys				
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Ala Ala Thr Glu Ile Leu Gln Leu Cys Phe Asp Ala Lys Asp Trp Lys				
35	40	45		
Leu Leu Asn Glu Gln Ile Leu Asn Leu Ser Lys Lys Arg Gly Gln Leu				
50	55	60		
Lys Gln Ala Val Gln Ser Met Val Gln Gln Ala Met Gln Tyr Ile Asp				
65	70	75	80	
Gln Thr Pro Asp Ile Glu Thr Arg Ile Glu Leu Ile Lys Thr Leu Asn				
85	90	95		
Asn Val Ser Ala Gly Lys Ile Tyr Val Glu Ile Glu Arg Ala Arg Leu				
100	105	110		
Thr Lys Lys Leu Ala Lys Ile Lys Glu Glu Gln Gly Gln Ile Ala Glu				
115	120	125		

Ala Ala Asp Leu Met Gln Glu Val Ala Val Glu Thr Phe Gly Ala Met
130 135 140

Ala Lys Thr Glu Lys Ile Ala Phe Ile Leu Glu Gln Val Arg Leu Cys
145 150 155 160

Leu Asp Arg Gln Asp Phe Val Arg Ala Gln Ile Leu Ser Arg Lys Ile
165 170 175

Asn Pro Arg Val Phe Asp Ala Asp Thr Lys Lys Asp Lys Lys Pro
180 185 190

Lys Glu Gly Asp Asn Met Val Glu Glu Ala Pro Ala Asp Ile Pro Thr
195 200 205

Leu Leu Glu Leu Lys Arg Ile Tyr Tyr Glu Leu Met Ile Arg Tyr Tyr
210 215 220

Ser His Asn Asn Glu Tyr Ile Glu Ile Cys Arg Ser Tyr Lys Ala Ile
225 230 235 240

Tyr Asp Ile Pro Ser Val Lys Glu Thr Pro Glu Gln Trp Ile Pro Val
245 250 255

Leu Arg Lys Ile Cys Trp Phe Leu Val Leu Ala Pro His Asp Pro Met
260 265 270

Gln Ser Ser Leu Leu Asn Ala Thr Leu Glu Asp Lys Asn Leu Ser Glu
275 280 285

Ile Pro Asp Phe Lys Met Leu Leu Lys Gln Val Val Thr Met Glu Val
290 295 300

Ile Gln Trp Thr Ser Leu Trp Asn Lys Tyr Lys Asp Glu Phe Glu Lys
305 310 315 320

Glu Lys Ser Met Ile Gly Gly Ser Leu Gly Asp Lys Ala Gly Glu Asp
325 330 335

Leu Lys Leu Arg Ile Ile Glu His Asn Ile Leu Val Val Ser Lys Tyr
340 345 350

Tyr Ala Arg Ile Thr Leu Lys Arg Leu Ala Glu Leu Leu Cys Leu Ser
355 360 365

Met Glu Glu Ala Glu Lys His Leu Ser Glu Met Val Val Ser Lys Ala
 370 375 380

Leu Ile Ala Lys Ile Asp Arg Pro Ser Gly Ile Val Cys Phe Gln Ile
 385 390 395 400

Ala Lys Asp Ser Asn Glu Ile Leu Asn Ser Trp Ala Gly Asn Leu Glu
 405 410 415

Lys Leu Leu Asp Leu Val Glu Lys Ser Cys His Gln Ile His Lys Glu
 420 425 430

Thr Met Val His Lys Ala Ala Leu Arg Pro
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<210> 79

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<212> DNA

<213> *Arabidopsis thaliana*

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cct tct ctg caa tta aga aag ccg gtg atg gcg gca gtg aaa gga gga 96
 Pro Ser Leu Gln Leu Arg Lys Pro Val Met Ala Ala Val Lys Gly Gly
 20 25 30

aaa caa tcg gtg aga aga agc agc aat acg gtg gtt cag ata acg tgt 144
 Lys Gln Ser Val Arg Arg Ser Ser Asn Thr Val Val Gln Ile Thr Cys
 35 40 45

cgt aag aag gaa ttg cat cct gaa ttc cac gaa gac gca aag gtt tac 192
 Arg Lys Lys Glu Leu His Pro Glu Phe His Glu Asp Ala Lys Val Tyr
 50 55 60

tgc aat gga gag ctg gtg atg act aca gga gga aca aag aaa gag tat 240
 Cys Asn Gly Glu Leu Val Met Thr Thr Gly Gly Thr Lys Lys Glu Tyr
 65 70 75 80

gtg gtt gat gta tgg tca ggt aac cat ccg ttt tac ctc ggg aat cgt	85	90	95	288
Val Val Asp Val Trp Ser Gly Asn His Pro Phe Tyr Leu Gly Asn Arg				
tcg gct ttg atg gtt gat gct gat caa gtt gag aag ttt cgt aag agg	100	105	110	336
Ser Ala Leu Met Val Asp Ala Asp Gln Val Glu Lys Phe Arg Lys Arg				
ttc gct ggg ctt tct gag att atg gag att cct gtg ctt aaa gga gaa	115	120	125	384
Phe Ala Gly Leu Ser Glu Ile Met Glu Ile Pro Val Leu Lys Gly Glu				
atc att atg cct act aag aaa agt aaa ggt ccc aaa ggg aag aag aaa	130	135	140	432
Ile Ile Met Pro Thr Lys Lys Ser Lys Gly Pro Lys Gly Lys Lys Lys				
tga				435

<210> 80

<211> 144

<212> PRT

<213> *Arabidopsis thaliana*

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Met Ala Val Ser Leu Pro Asn Ser Phe Leu Gln Ile Ser Pro Cys Val	1	5	10	15
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Pro Ser Leu Gln Leu Arg Lys Pro Val Met Ala Ala Val Lys Gly Gly	20	25	30
---	----	----	----

Lys Gln Ser Val Arg Arg Ser Ser Asn Thr Val Val Gln Ile Thr Cys	35	40	45
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Arg Lys Lys Glu Leu His Pro Glu Phe His Glu Asp Ala Lys Val Tyr	50	55	60
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Cys Asn Gly Glu Leu Val Met Thr Thr Gly Gly Thr Lys Lys Glu Tyr	65	70	75	80
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Val Val Asp Val Trp Ser Gly Asn His Pro Phe Tyr Leu Gly Asn Arg	85	90	95
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Ser Ala Leu Met Val Asp Ala Asp Gln Val Glu Lys Phe Arg Lys Arg	100	105	110
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Phe Ala Gly Leu Ser Glu Ile Met Glu Ile Pro Val Leu Lys Gly Glu
 115 120 125

Ile Ile Met Pro Thr Lys Lys Ser Lys Gly Pro Lys Gly Lys Lys Lys
 130 135 140

<210> 81

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Met Ala Trp Ser Ile Ala Leu Leu Thr Pro Pro Phe Phe Gly Pro Gly		
1 5 10 15		
agg cat gtg cag gcc aaa gaa tac agg gaa cca aga ggg tgt gtg atg		96
Arg His Val Gln Ala Lys Glu Tyr Arg Glu Pro Arg Gly Cys Val Met		
20 25 30		
aag atg agc agt tta aaa gca cct gtt ctg aga att cag gcc aca gaa		144
Lys Met Ser Ser Leu Lys Ala Pro Val Leu Arg Ile Gln Ala Thr Glu		
35 40 45		
tac aga gaa cca aga ggg cgt gtg aag atg atg tcc agt tta caa gca		192
Tyr Arg Glu Pro Arg Gly Arg Val Lys Met Ser Ser Leu Gln Ala		
50 55 60		
cct ctt ctg aca att cag agc ttc tca ggg tta agg gcc ccc agt gca		240
Pro Leu Leu Thr Ile Gln Ser Phe Ser Gly Leu Arg Ala Pro Ser Ala		
65 70 75 80		
tta gat tat ttg gga agg cct agt cca ggt ttc ctt gtt aag tat aaa		288
Leu Asp Tyr Leu Gly Arg Pro Ser Pro Gly Phe Leu Val Lys Tyr Lys		
85 90 95		
ctt gca aaa tca tct ggg aga gaa aaa gct agc cga tgt gta ccc aaa		336
Leu Ala Lys Ser Ser Gly Arg Glu Lys Ala Ser Arg Cys Val Pro Lys		
100 105 110		
gca atg ttt gag cgt ttt acc gag aaa gca att aag gtc ata atg ctg		384
Ala Met Phe Glu Arg Phe Thr Glu Lys Ala Ile Lys Val Ile Met Leu		
115 120 125		

tct caa gag gaa gct cgg aga ctt ggc cat aac ttt gtt ggg act gag	130	135	140	432
Ser Gln Glu Glu Ala Arg Arg Leu Gly His Asn Phe Val Gly Thr Glu				
caa ata ctg ttg ggt cta att gga gaa ggg act ggg att gcc gcc aag	145	150	155	480
Gln Ile Leu Leu Gly Leu Ile Gly Glu Gly Thr Gly Ile Ala Ala Lys				
gtt ctt aaa tcc atg ggg atc aat ctt aaa gat tca cgc gtg gaa gta	165	170	175	528
Val Leu Lys Ser Met Gly Ile Asn Leu Lys Asp Ser Arg Val Glu Val				
gaa aag ata att ggg aga ggc agt gga ttc gtg gca gtg gag att cca	180	185	190	576
Glu Lys Ile Ile Gly Arg Gly Ser Gly Phe Val Ala Val Glu Ile Pro				
ttt act cct cgc gca aag cgg gtg ctg gag ttg tca cta gag gaa gct	195	200	205	624
Phe Thr Pro Arg Ala Lys Arg Val Leu Glu Leu Ser Leu Glu Glu Ala				
cga caa ctt ggg cat aac tac att ggt tca gag cac ctt ttg ctt ggt	210	215	220	672
Arg Gln Leu Gly His Asn Tyr Ile Gly Ser Glu His Leu Leu Leu Gly				
cta ctt cgt gaa ggg gag ggt gtg gca gct cgt gtc ttg gag aat ttg	225	230	235	720
Leu Leu Arg Glu Gly Glu Gly Val Ala Ala Arg Val Leu Glu Asn Leu				
ggt gca gat cct agt aat ata cgg aca cag gtt ata cgt atg gtc ggg	245	250	255	768
Gly Ala Asp Pro Ser Asn Ile Arg Thr Gln Val Ile Arg Met Val Gly				
gaa aac aat gaa gtc aca gca agc gtt ggt ggg gga agc agc gga aac	260	265	270	816
Glu Asn Asn Glu Val Thr Ala Ser Val Gly Gly Ser Ser Gly Asn				
agc aaa atg cca aca ctt gaa gag tat ggg act aac tta act aaa cta	275	280	285	864
Ser Lys Met Pro Thr Leu Glu Glu Tyr Thr Asn Leu Thr Lys Leu				
gca gag gag ggt aaa ctg gat ccg gtt gtt gga agg cag cca cag atc	290	295	300	912
Ala Glu Glu Gly Lys Leu Asp Pro Val Val Gly Arg Gln Pro Gln Ile				
gaa cga atg gtc cag atc ttg gct cga aga acc aag aac aac cca tgt	305	310	315	960
Glu Arg Met Val Gln Ile Leu Ala Arg Arg Thr Lys Asn Asn Pro Cys				
ctt att gga gaa cct gga gtt ggt aag acg gca ata gca gaa gga ctt	325	330	335	1008
Leu Ile Gly Glu Pro Gly Val Gly Lys Thr Ala Ile Ala Glu Gly Leu				
gca cag cga ata gct agt ggt gat gtt cct gaa aca atc gag ggg aag	340	345	350	1056
Ala Gln Arg Ile Ala Ser Gly Asp Val Pro Glu Thr Ile Glu Gly Lys				
acg gtt ata acc ctt gat atg ggt ctt cta gtg gct gga acg aaa tac	355	360	365	1104
Thr Val Ile Thr Leu Asp Met Gly Leu Leu Val Ala Gly Thr Lys Tyr				

cgt gga gag ttc gag gaa aga ttg aag aag ctt atg gag gaa atc agg Arg Gly Phe Glu Glu Arg Leu Lys Lys Leu Met Glu Glu Ile Arg 370 375 380	1152
caa agt gat gag ata att ctg ttt att gat gaa gtg cac acg ctc atc Gln Ser Asp Glu Ile Ile Leu Phe Ile Asp Glu Val His Thr Leu Ile 385 390 395 400	1200
ggt gca gga gcc gct gaa ggt gcg atc gat gct gct aac atc tta aag Gly Ala Gly Ala Ala Glu Gly Ala Ile Asp Ala Ala Asn Ile Leu Lys 405 410 415	1248
cca gct cta gca aga ggt gaa ttg cag tgt att ggt gca aca aca att Pro Ala Leu Ala Arg Gly Glu Leu Gln Cys Ile Gly Ala Thr Thr Ile 420 425 430	1296
gat gag tac agg aaa cac att gag aaa gat cct gca ttg gag aga cgg Asp Glu Tyr Arg Lys His Ile Glu Lys Asp Pro Ala Leu Glu Arg Arg 435 440 445	1344
ttc cag cct gtg aaa gta cct gaa cca act gta gaa gaa gct ata cag Phe Gln Pro Val Lys Val Pro Glu Pro Thr Val Glu Glu Ala Ile Gln 450 455 460	1392
att ttg caa ggt ctg cgt gag cgc tat gag atc cac cac aaa ctt cga Ile Leu Gln Gly Leu Arg Glu Arg Tyr Glu Ile His His Lys Leu Arg 465 470 475 480	1440
tac act gat gaa gcc ttg gtt gct gct gca caa ttg tca cat cag tac Tyr Thr Asp Glu Ala Leu Val Ala Ala Gln Leu Ser His Gln Tyr 485 490 495	1488
atc agt gat cgg ttt ctt ccc gac aaa gcg att gac ttg att gat gaa Ile Ser Asp Arg Phe Leu Pro Asp Lys Ala Ile Asp Leu Ile Asp Glu 500 505 510	1536
gct ggg tct cgg gtt cga cta cgc cat gct cag ctt cct gag gaa gct Ala Gly Ser Arg Val Arg Leu Arg His Ala Gln Leu Pro Glu Glu Ala 515 520 525	1584
aga gag ctt gaa aag caa ctc agg caa atc acc aaa gag aag aat gaa Arg Glu Leu Glu Lys Gln Leu Arg Gln Ile Thr Lys Glu Lys Asn Glu 530 535 540	1632
gct gtg cga agc caa gac ttc gag atg gct ggt tct cat cgt gac cgt Ala Val Arg Ser Gln Asp Phe Glu Met Ala Gly Ser His Arg Asp Arg 545 550 555 560	1680
gaa ata gag ctc aag gct gag ata gct aat gtt tta tct cga ggc aaa Glu Ile Glu Leu Lys Ala Glu Ile Ala Asn Val Leu Ser Arg Gly Lys 565 570 575	1728
gaa gtg gcc aaa gcc gag aat gaa gct gag gaa gga gga cct act gtc Glu Val Ala Lys Ala Glu Asn Glu Ala Glu Glu Gly Gly Pro Thr Val 580 585 590	1776
aca gaa tct gac atc caa cac atc gtc gcc acc tgg aca gga atc ccg Thr Glu Ser Asp Ile Gln His Ile Val Ala Thr Trp Thr Gly Ile Pro 595 600 605	1824

gta gag aaa gtc tcg tct gat gaa tct agc cgt ctt ctc caa atg gag	610	615	620	1872
Val Glu Lys Val Ser Ser Asp Glu Ser Ser Arg Leu Leu Gln Met Glu				
cag acc ctt cac aca aga gtc att ggc caa gat gaa gcc gtt aaa gca	625	630	635	1920
Gln Thr Leu His Thr Arg Val Ile Gly Gln Asp Glu Ala Val Lys Ala				
atc agt cgg gct atc cgc cgt gcc cgt gtt ggg ctc aaa aac cca aac	645	650	655	1968
Ile Ser Arg Ala Ile Arg Arg Ala Arg Val Gly Leu Lys Asn Pro Asn				
cgt cct atc gcc agt ttc atc ttc tct ggt cca act ggt gtt ggg aaa	660	665	670	2016
Arg Pro Ile Ala Ser Phe Ile Phe Ser Gly Pro Thr Gly Val Gly Lys				
tca gag ctt gct aag gcc ttg gct gct tac tac ttc ggt tca gaa gaa	675	680	685	2064
Ser Glu Leu Ala Lys Ala Leu Ala Tyr Tyr Phe Gly Ser Glu Glu				
gca atg atc cgt ctt gac atg agt gag ttc atg gaa cga cac act gtt	690	695	700	2112
Ala Met Ile Arg Leu Asp Met Ser Glu Phe Met Glu Arg His Thr Val				
tcg aaa ctc atc ggt tca cct ggt tac gta gga tac aca gaa gga	705	710	715	2160
Ser Lys Leu Ile Gly Ser Pro Pro Gly Tyr Val Gly Tyr Thr Glu Gly				
ggt cag tta aca gag gcg gtt cga cgc agg ccc tac act ctt gtt ctc	725	730	735	2208
Gly Gln Leu Thr Glu Ala Val Arg Arg Pro Tyr Thr Leu Val Leu				
ttt gac gaa att gag aaa gca cat ccc gat gtt ttc aac atg atg ctt	740	745	750	2256
Phe Asp Glu Ile Glu Lys Ala His Pro Asp Val Phe Asn Met Met Leu				
cag atc cta gaa gac ggt aga cta act gat agc aaa gga aga act gtc	755	760	765	2304
Gln Ile Leu Glu Asp Gly Arg Leu Thr Asp Ser Lys Gly Arg Thr Val				
gat ttc aag aac acg ctt ctg atc atg act tca aac gta ggg agc agc	770	775	780	2352
Asp Phe Lys Asn Thr Leu Leu Ile Met Thr Ser Asn Val Gly Ser Ser				
gtg atc gaa aaa ggt ggt aga aga att ggg ttt gat ctt gac cac gac	785	790	795	2400
Val Ile Glu Lys Gly Gly Arg Arg Ile Gly Phe Asp Leu Asp His Asp				
gag aaa gac agc agt tac aac aga atc aag agc tta gtg act gag gaa	805	810	815	2448
Glu Lys Asp Ser Ser Tyr Asn Arg Ile Lys Ser Leu Val Thr Glu Glu				
cta aaa cag tat ttc aga cca gag ttc ttg aac agg tta gat gag atg	820	825	830	2496
Leu Lys Gln Tyr Phe Arg Pro Glu Phe Leu Asn Arg Leu Asp Glu Met				
att gtt ttc aga cag tta aca aag ctg gaa gtc aag gag att gct gat	835	840	845	2544
Ile Val Phe Arg Gln Leu Thr Lys Leu Glu Val Lys Glu Ile Ala Asp				

ata atg ctt aaa gaa gtg gtg gcg aga ctt gag gtc aaa gag att gag 2592
 Ile Met Leu Lys Glu Val Val Ala Arg Leu Glu Val Lys Glu Ile Glu
 850 855 860

ctt cag gtg act gag agg ttt aaa gag aga gtg gtg gat gaa gga ttc 2640
 Leu Gln Val Thr Glu Arg Phe Lys Glu Arg Val Val Asp Glu Gly Phe
 865 870 875 880

gac ccg agt tat ggt gcg agg cca ctt aga cgt gca ata atg agg ctt 2688
 Asp Pro Ser Tyr Gly Ala Arg Pro Leu Arg Arg Ala Ile Met Arg Leu
 885 890 895

ttg gag gat agt atg gcg gag aag atg ctt tca agg gac att aaa gaa 2736
 Leu Glu Asp Ser Met Ala Glu Lys Met Leu Ser Arg Asp Ile Lys Glu
 900 905 910

gga gat tct gtg att gtt gat gtt gat gcc gaa gga agt gtg gtt gtg 2784
 Gly Asp Ser Val Ile Val Asp Val Asp Ala Glu Gly Ser Val Val Val
 915 920 925

ttg agt ggt acc act gga cgt gtt ggt ggt ttt gct gct gaa gaa gcc 2832
 Leu Ser Gly Thr Thr Gly Arg Val Gly Gly Phe Ala Ala Glu Glu Ala
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 Met Glu Asp Pro Ile Pro Ile Leu
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<212> PRT

<213> *Arabidopsis thaliana*

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Arg His Val Gln Ala Lys Glu Tyr Arg Glu Pro Arg Gly Cys Val Met
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Lys Met Ser Ser Leu Lys Ala Pro Val Leu Arg Ile Gln Ala Thr Glu
 35 40 45

Tyr Arg Glu Pro Arg Gly Arg Val Lys Met Met Ser Ser Leu Gln Ala
 50 55 60

Pro Leu Leu Thr Ile Gln Ser Phe Ser Gly Leu Arg Ala Pro Ser Ala
 65 70 75 80

Leu Asp Tyr Leu Gly Arg Pro Ser Pro Gly Phe Leu Val Lys Tyr Lys
85 90 95

Leu Ala Lys Ser Ser Gly Arg Glu Lys Ala Ser Arg Cys Val Pro Lys
100 105 110

Ala Met Phe Glu Arg Phe Thr Glu Lys Ala Ile Lys Val Ile Met Leu
115 120 125

Ser Gln Glu Glu Ala Arg Arg Leu Gly His Asn Phe Val Gly Thr Glu
130 135 140

Gln Ile Leu Leu Gly Leu Ile Gly Glu Gly Thr Gly Ile Ala Ala Lys
145 150 155 160

Val Leu Lys Ser Met Gly Ile Asn Leu Lys Asp Ser Arg Val Glu Val
165 170 175

Glu Lys Ile Ile Gly Arg Gly Ser Gly Phe Val Ala Val Glu Ile Pro
180 185 190

Phe Thr Pro Arg Ala Lys Arg Val Leu Glu Leu Ser Leu Glu Glu Ala
195 200 205

Arg Gln Leu Gly His Asn Tyr Ile Gly Ser Glu His Leu Leu Leu Gly
210 215 220

Leu Leu Arg Glu Gly Glu Gly Val Ala Ala Arg Val Leu Glu Asn Leu
225 230 235 240

Gly Ala Asp Pro Ser Asn Ile Arg Thr Gln Val Ile Arg Met Val Gly
245 250 255

Glu Asn Asn Glu Val Thr Ala Ser Val Gly Gly Ser Ser Gly Asn
260 265 270

Ser Lys Met Pro Thr Leu Glu Glu Tyr Gly Thr Asn Leu Thr Lys Leu
275 280 285

Ala Glu Glu Gly Lys Leu Asp Pro Val Val Gly Arg Gln Pro Gln Ile
290 295 300

Glu Arg Met Val Gln Ile Leu Ala Arg Arg Thr Lys Asn Asn Pro Cys
305 310 315 320

Leu Ile Gly Glu Pro Gly Val Gly Lys Thr Ala Ile Ala Glu Gly Leu
325 330 335

Ala Gln Arg Ile Ala Ser Gly Asp Val Pro Glu Thr Ile Glu Gly Lys
340 345 350

Thr Val Ile Thr Leu Asp Met Gly Leu Leu Val Ala Gly Thr Lys Tyr
355 360 365

Arg Gly Glu Phe Glu Glu Arg Leu Lys Lys Leu Met Glu Glu Ile Arg
370 375 380

Gln Ser Asp Glu Ile Ile Leu Phe Ile Asp Glu Val His Thr Leu Ile
385 390 395 400

Gly Ala Gly Ala Ala Glu Gly Ala Ile Asp Ala Ala Asn Ile Leu Lys
405 410 415

Pro Ala Leu Ala Arg Gly Glu Leu Gln Cys Ile Gly Ala Thr Thr Ile
420 425 430

Asp Glu Tyr Arg Lys His Ile Glu Lys Asp Pro Ala Leu Glu Arg Arg
435 440 445

Phe Gln Pro Val Lys Val Pro Glu Pro Thr Val Glu Glu Ala Ile Gln
450 455 460

Ile Leu Gln Gly Leu Arg Glu Arg Tyr Glu Ile His His Lys Leu Arg
465 470 475 480

Tyr Thr Asp Glu Ala Leu Val Ala Ala Gln Leu Ser His Gln Tyr
485 490 495

Ile Ser Asp Arg Phe Leu Pro Asp Lys Ala Ile Asp Leu Ile Asp Glu
500 505 510

Ala Gly Ser Arg Val Arg Leu Arg His Ala Gln Leu Pro Glu Glu Ala
515 520 525

Arg Glu Leu Glu Lys Gln Leu Arg Gln Ile Thr Lys Glu Lys Asn Glu
530 535 540

Ala Val Arg Ser Gln Asp Phe Glu Met Ala Gly Ser His Arg Asp Arg
545 550 555 560

Glu Ile Glu Leu Lys Ala Glu Ile Ala Asn Val Leu Ser Arg Gly Lys
565 570 575

Glu Val Ala Lys Ala Glu Asn Glu Ala Glu Gly Gly Pro Thr Val
580 585 590

Thr Glu Ser Asp Ile Gln His Ile Val Ala Thr Trp Thr Gly Ile Pro
595 600 605

Val Glu Lys Val Ser Ser Asp Glu Ser Ser Arg Leu Leu Gln Met Glu
610 615 620

Gln Thr Leu His Thr Arg Val Ile Gly Gln Asp Glu Ala Val Lys Ala
625 630 635 640

Ile Ser Arg Ala Ile Arg Arg Ala Arg Val Gly Leu Lys Asn Pro Asn
645 650 655

Arg Pro Ile Ala Ser Phe Ile Phe Ser Gly Pro Thr Gly Val Gly Lys
660 665 670

Ser Glu Leu Ala Lys Ala Leu Ala Ala Tyr Tyr Phe Gly Ser Glu Glu
675 680 685

Ala Met Ile Arg Leu Asp Met Ser Glu Phe Met Glu Arg His Thr Val
690 695 700

Ser Lys Leu Ile Gly Ser Pro Pro Gly Tyr Val Gly Tyr Thr Glu Gly
705 710 715 720

Gly Gln Leu Thr Glu Ala Val Arg Arg Pro Tyr Thr Leu Val Leu
725 730 735

Phe Asp Glu Ile Glu Lys Ala His Pro Asp Val Phe Asn Met Met Leu
740 745 750

Gln Ile Leu Glu Asp Gly Arg Leu Thr Asp Ser Lys Gly Arg Thr Val
755 760 765

Asp Phe Lys Asn Thr Leu Leu Ile Met Thr Ser Asn Val Gly Ser Ser
770 775 780

Val Ile Glu Lys Gly Gly Arg Arg Ile Gly Phe Asp Leu Asp His Asp
785 790 795 800

Glu Lys Asp Ser Ser Tyr Asn Arg Ile Lys Ser Leu Val Thr Glu Glu
805 810 815

Leu Lys Gln Tyr Phe Arg Pro Glu Phe Leu Asn Arg Leu Asp Glu Met
820 825 830

Ile Val Phe Arg Gln Leu Thr Lys Leu Glu Val Lys Glu Ile Ala Asp
835 840 845

Ile Met Leu Lys Glu Val Val Ala Arg Leu Glu Val Lys Glu Ile Glu
850 855 860

Leu Gln Val Thr Glu Arg Phe Lys Glu Arg Val Val Asp Glu Gly Phe
865 870 875 880

Asp Pro Ser Tyr Gly Ala Arg Pro Leu Arg Arg Ala Ile Met Arg Leu
885 890 895

Leu Glu Asp Ser Met Ala Glu Lys Met Leu Ser Arg Asp Ile Lys Glu
900 905 910

Gly Asp Ser Val Ile Val Asp Val Asp Ala Glu Gly Ser Val Val Val
915 920 925

Leu Ser Gly Thr Thr Gly Arg Val Gly Gly Phe Ala Ala Glu Glu Ala
930 935 940

Met Glu Asp Pro Ile Pro Ile Leu
945 950

<210> 83

<211> 1467

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (1) .. (1467)

<223> 65310

<400> 83
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 Met Thr Gln Asp Val Glu Met Lys Asp Asn Asn Thr Pro Ser Gln Ser
 1 5 10 15

att atc tct tct tct acc tct act atg cag aat ttg aag gag att gca 96
 Ile Ile Ser Ser Ser Thr Ser Thr Met Gln Asn Leu Lys Glu Ile Ala
 20 25 30

gca ctc atc gat act ggg tct tac acg aag gag gtt cgt cgt att gct 144
 Ala Leu Ile Asp Thr Gly Ser Tyr Thr Lys Glu Val Arg Arg Ile Ala
 35 40 45

cgt gct gtg cgt ctc act ata ggg ctt agg cag aaa ctc acc ggc tct 192
 Arg Ala Val Arg Leu Thr Ile Gly Leu Arg Gln Lys Leu Thr Gly Ser
 50 55 60

gtg ctc tct tcc ttc ctg gat ttt gct ttg gtt cca gga tcc gaa gct 240
 Val Leu Ser Ser Phe Leu Asp Phe Ala Leu Val Pro Gly Ser Glu Ala
 65 70 75 80

cac tct cgc ctc tct tcc ttt gtt cct aag ggt gat gaa cat gac atg 288
 His Ser Arg Leu Ser Ser Phe Val Pro Lys Gly Asp Glu His Asp Met
 85 90 95

gaa gtt gat act gcc tca tcg gcc aca caa gct gct cct tct aag cat 336
 Glu Val Asp Thr Ala Ser Ser Ala Thr Gln Ala Ala Pro Ser Lys His
 100 105 110

cta cct gca gag ctc gag atc tac tgc tac ttc att gtt ctt ctt ttt 384
 Leu Pro Ala Glu Leu Glu Ile Tyr Cys Tyr Phe Ile Val Leu Leu Phe
 115 120 125

ctg att gat cag aag aag tac aac gag gct aaa gct tgt tct tca gca 432
 Leu Ile Asp Gln Lys Lys Tyr Asn Glu Ala Lys Ala Cys Ser Ser Ala
 130 135 140

agc att gct cgt ctc aag aac gtc aac cga agg acc att gat gtg ata 480
 Ser Ile Ala Arg Leu Lys Asn Val Asn Arg Arg Thr Ile Asp Val Ile
 145 150 155 160

gca tca aga ctc tac ttt tac tat tct ttg agt tat gag caa acc ggt 528
 Ala Ser Arg Leu Tyr Phe Tyr Ser Leu Ser Tyr Glu Gln Thr Gly
 165 170 175

gat ctt gct gaa att cgc ggt act ctt ctt gcg ttg cat cat tct gca 576
 Asp Leu Ala Glu Ile Arg Gly Thr Leu Leu Ala Leu His His Ser Ala
 180 185 190

acg cta aga cac gat gag ctg ggt cag gaa acc ctt ctg aac ctg ttg 624
 Thr Leu Arg His Asp Glu Leu Gly Gln Glu Thr Leu Leu Asn Leu Leu
 195 200 205

cta cgt aac tat ttg cat tac aac ctc tat gat cag gca gag aag cta 672
 Leu Arg Asn Tyr Leu His Tyr Asn Leu Tyr Asp Gln Ala Glu Lys Leu
 210 215 220

aga tca aag gca cct cgc ttt gag gct cat tca aac caa cag ttt tgt 720

Arg Ser Lys Ala Pro Arg Phe Glu Ala His Ser Asn Gln Gln Phe Cys			
225	230	235	240
agg tac ctt ttc tat ctc ggg aag att cgt act att cag ctc gaa tat			768
Arg Tyr Leu Phe Tyr Leu Gly Lys Ile Arg Thr Ile Gln Leu Glu Tyr			
245	250	255	
acg gac gca aaa gag agc ctt ctt cag gcg gcc agg aaa gcc cct ata			816
Thr Asp Ala Lys Glu Ser Leu Leu Gln Ala Ala Arg Lys Ala Pro Ile			
260	265	270	
gca gct ttg ggc ttc agg atc caa tgc aat aaa tgg gca att ctg gtt			864
Ala Ala Leu Gly Phe Arg Ile Gln Cys Asn Lys Trp Ala Ile Leu Val			
275	280	285	
cgt cta ctg ctg ggt gag ata cca gag cgt tct atc ttc act caa aag			912
Arg Leu Leu Leu Gly Glu Ile Pro Glu Arg Ser Ile Phe Thr Gln Lys			
290	295	300	
ggt atg gag aag gcc ctc aga ccc tac ttc gag cta aca aat gcg gtt			960
Gly Met Glu Lys Ala Leu Arg Pro Tyr Phe Glu Leu Thr Asn Ala Val			
305	310	315	320
agg att ggg gac ttg gag ttg ttt agg aca gtc cag gag aag ttc ttg			1008
Arg Ile Gly Asp Leu Glu Leu Phe Arg Thr Val Gln Glu Lys Phe Leu			
325	330	335	
gac aca ttt gct caa gac aga acg cac aat ctc atc gtg cga ctc cgc			1056
Asp Thr Phe Ala Gln Asp Arg Thr His Asn Leu Ile Val Arg Leu Arg			
340	345	350	
cac aat gtc atc agg act gga ctg cgg aac ata agt atc tcc tac tca			1104
His Asn Val Ile Arg Thr Gly Leu Arg Asn Ile Ser Tyr Ser			
355	360	365	
aga atc tct tta ccc gat gtt gcc aaa aag ctg agg ctc aac tct gaa			1152
Arg Ile Ser Leu Pro Asp Val Ala Lys Lys Leu Arg Leu Asn Ser Glu			
370	375	380	
aac cct gtg gct gat gcg gaa agc atc gtg gca aag gcc ata cgc gac			1200
Asn Pro Val Ala Asp Ala Glu Ser Ile Val Ala Lys Ala Ile Arg Asp			
385	390	395	400
gga gct att gat gct aca atc gat cac aaa aac gga tgc atg gtc tcc			1248
Gly Ala Ile Asp Ala Thr Ile Asp His Lys Asn Gly Cys Met Val Ser			
405	410	415	
aaa gaa act ggg gac atc tac tcg acg aat gag cca caa act gcg ttc			1296
Lys Glu Thr Gly Asp Ile Tyr Ser Thr Asn Glu Pro Gln Thr Ala Phe			
420	425	430	
aac tca aga att gct ttc tgc ctc aac atg cat aac gaa gct gtc aga			1344
Asn Ser Arg Ile Ala Phe Cys Leu Asn Met His Asn Glu Ala Val Arg			
435	440	445	
gca ttg agg ttt cct aac act cac aag gag aaa gaa agc gat gag			1392
Ala Leu Arg Phe Pro Pro Asn Thr His Lys Glu Lys Ser Asp Glu			
450	455	460	
aag agg aga gag agg aag caa cag gaa gaa gag ctt gct aag cat atg			1440

Lys Arg Arg Glu Arg Lys Gln Gln Glu Glu Glu Leu Ala Lys His Met
465 470 475 480

gct gag gaa gac gat gat gat ttt tag 1467
Ala Glu Glu Asp Asp Asp Asp Phe
485

<210> 84

<211> 488

<212> PRT

<213> *Arabidopsis thaliana*

<400> 84

Met Thr Gln Asp Val Glu Met Lys Asp Asn Asn Thr Pro Ser Gln Ser
1 5 10 15

Ile Ile Ser Ser Ser Thr Ser Thr Met Gln Asn Leu Lys Glu Ile Ala
20 25 30

Ala Leu Ile Asp Thr Gly Ser Tyr Thr Lys Glu Val Arg Arg Ile Ala
35 40 45

Arg Ala Val Arg Leu Thr Ile Gly Leu Arg Gln Lys Leu Thr Gly Ser
50 55 60

Val Leu Ser Ser Phe Leu Asp Phe Ala Leu Val Pro Gly Ser Glu Ala
65 70 75 80

His Ser Arg Leu Ser Ser Phe Val Pro Lys Gly Asp Glu His Asp Met
85 90 95

Glu Val Asp Thr Ala Ser Ser Ala Thr Gln Ala Ala Pro Ser Lys His
100 105 110

Leu Pro Ala Glu Leu Glu Ile Tyr Cys Tyr Phe Ile Val Leu Leu Phe
115 120 125

Leu Ile Asp Gln Lys Lys Tyr Asn Glu Ala Lys Ala Cys Ser Ser Ala
130 135 140

Ser Ile Ala Arg Leu Lys Asn Val Asn Arg Arg Thr Ile Asp Val Ile
145 150 155 160

Ala Ser Arg Leu Tyr Phe Tyr Tyr Ser Leu Ser Tyr Glu Gln Thr Gly
165 170 175

Asp Leu Ala Glu Ile Arg Gly Thr Leu Leu Ala Leu His His Ser Ala
180 185 190

Thr Leu Arg His Asp Glu Leu Gly Gln Glu Thr Leu Leu Asn Leu Leu
195 200 205

Leu Arg Asn Tyr Leu His Tyr Asn Leu Tyr Asp Gln Ala Glu Lys Leu
210 215 220

Arg Ser Lys Ala Pro Arg Phe Glu Ala His Ser Asn Gln Gln Phe Cys
225 230 235 240

Arg Tyr Leu Phe Tyr Leu Gly Lys Ile Arg Thr Ile Gln Leu Glu Tyr
245 250 255

Thr Asp Ala Lys Glu Ser Leu Leu Gln Ala Ala Arg Lys Ala Pro Ile
260 265 270

Ala Ala Leu Gly Phe Arg Ile Gln Cys Asn Lys Trp Ala Ile Leu Val
275 280 285

Arg Leu Leu Leu Gly Glu Ile Pro Glu Arg Ser Ile Phe Thr Gln Lys
290 295 300

Gly Met Glu Lys Ala Leu Arg Pro Tyr Phe Glu Leu Thr Asn Ala Val
305 310 315 320

Arg Ile Gly Asp Leu Glu Leu Phe Arg Thr Val Gln Glu Lys Phe Leu
325 330 335

Asp Thr Phe Ala Gln Asp Arg Thr His Asn Leu Ile Val Arg Leu Arg
340 345 350

His Asn Val Ile Arg Thr Gly Leu Arg Asn Ile Ser Ile Ser Tyr Ser
355 360 365

Arg Ile Ser Leu Pro Asp Val Ala Lys Lys Leu Arg Leu Asn Ser Glu
370 375 380

Asn Pro Val Ala Asp Ala Glu Ser Ile Val Ala Lys Ala Ile Arg Asp
385 390 395 400

Gly Ala Ile Asp Ala Thr Ile Asp His Lys Asn Gly Cys Met Val Ser
 405 410 415

Lys Glu Thr Gly Asp Ile Tyr Ser Thr Asn Glu Pro Gln Thr Ala Phe
 420 425 430

Asn Ser Arg Ile Ala Phe Cys Leu Asn Met His Asn Glu Ala Val Arg
 435 440 445

Ala Leu Arg Phe Pro Pro Asn Thr His Lys Glu Lys Glu Ser Asp Glu
 450 455 460

Lys Arg Arg Glu Arg Lys Gln Gln Glu Glu Leu Ala Lys His Met
 465 470 475 480

Ala Glu Glu Asp Asp Asp Asp Phe
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<210> 85

<211> 282

<212> DNA

<213> *Arabidopsis thaliana*

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<221> CDS

<222> (1)..(282)

<223> 68181

<400> 85
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 Met Asp Ala Ser Met Met Ala Gly Leu Asp Gly Leu Pro Glu Glu Asp
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aaa gcc aaa atg gcc tcc atg atc gat cag ctt cag ctc cgt gat agt 96
 Lys Ala Lys Met Ala Ser Met Ile Asp Gln Leu Gln Leu Arg Asp Ser
 20 25 30

ttg agg atg tac aat tca ttg gtg gag agg tgt ttc gtg gac tgt gtt 144
 Leu Arg Met Tyr Asn Ser Leu Val Glu Arg Cys Phe Val Asp Cys Val
 35 40 45

gat agc ttc aca cgc aaa tct ctg cag aaa caa gag gag act tgt gtg 192
 Asp Ser Phe Thr Arg Lys Ser Leu Gln Lys Glu Glu Thr Cys Val
 50 55 60

atg cgt tgc gct gag aag ttc ctt aag cat acg atg cgt gtt ggt atg 240
 Met Arg Cys Ala Glu Lys Phe Leu Lys His Thr Met Arg Val Gly Met
 65 70 75 80

cgg ttt gct gag ctc aat cag aac gca cca acc caa gac tga 282
 Arg Phe Ala Glu Leu Asn Gln Asn Ala Pro Thr Gln Asp
 85 90

<210> 86

<211> 93

<212> PRT

<213> *Arabidopsis thaliana*

<400> 86

Met Asp Ala Ser Met Met Ala Gly Leu Asp Gly Leu Pro Glu Glu Asp 1 5 10 15

Lys Ala Lys Met Ala Ser Met Ile Asp Gln Leu Gln Leu Arg Asp Ser 20 25 30

Leu Arg Met Tyr Asn Ser Leu Val Glu Arg Cys Phe Val Asp Cys Val 35 40 45

Asp Ser Phe Thr Arg Lys Ser Leu Gln Lys Gln Glu Glu Thr Cys Val 50 55 60

Met Arg Cys Ala Glu Lys Phe Leu Lys His Thr Met Arg Val Gly Met 65 70 75 80

Arg Phe Ala Glu Leu Asn Gln Asn Ala Pro Thr Gln Asp 85 90

<210> 87

<211> 816

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (1)..(816)

<223> 70913

<400> 87
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 Met Gln Ser Lys Pro Gly Arg Glu Asn Glu Glu Glu Val Asn Asn His
 1 5 10 15

 cat gct gtt cag cag ccg atg atg tat gca gag ccc tgg tgg aaa aac 96
 His Ala Val Gln Gln Pro Met Met Tyr Ala Glu Pro Trp Trp Lys Asn
 20 25 30

 aac tcc ttt ggt gtt gta cct caa gcg aga cct tct gga att cca tca 144
 Asn Ser Phe Gly Val Val Pro Gln Ala Arg Pro Ser Gly Ile Pro Ser
 35 40 45

 aat tcc tct tct ttg gat tgc ccc aat ggt tcc gag tca aac gat gtt 192
 Asn Ser Ser Ser Leu Asp Cys Pro Asn Gly Ser Glu Ser Asn Asp Val
 50 55 60

 cat tca gca tct gaa gac ggt gcg ttg aat ggt gaa aac gat ggc act 240
 His Ser Ala Ser Glu Asp Gly Ala Leu Asn Gly Glu Asn Asp Gly Thr
 65 70 75 80

 tgg aag gat tca caa gct gca act tcc tct cgt tca gat aat cac gga 288
 Trp Lys Asp Ser Gln Ala Ala Thr Ser Ser Arg Ser Asp Asn His Gly
 85 90 95

 atg gaa gga aat gac cca gcg ctc tct atc cgt aac atg cat gat cag 336
 Met Glu Gly Asn Asp Pro Ala Leu Ser Ile Arg Asn Met His Asp Gln
 100 105 110

 cca ctt gta caa cca cca gag ctt gtt gga cac tat atc gct tgt gtc 384
 Pro Leu Val Gln Pro Pro Glu Leu Val Gly His Tyr Ile Ala Cys Val
 115 120 125

 cca aac cca tat cag gat cca tat tat ggg gga ttg atg gga gca tat 432
 Pro Asn Pro Tyr Gln Asp Pro Tyr Tyr Gly Gly Leu Met Gly Ala Tyr
 130 135 140

 ggt cat cag caa ttg ggt ttt cgt cca tat ctt gga atg cct cgt gaa 480
 Gly His Gln Gln Leu Gly Phe Arg Pro Tyr Leu Gly Met Pro Arg Glu
 145 150 155 160

 aga aca gct ctg cca ctt gac atg gca caa gag ccc gtt tat gtg aat 528
 Arg Thr Ala Leu Pro Leu Asp Met Ala Gln Glu Pro Val Tyr Val Asn
 165 170 175

 gca aag cag tac gag gga att cta agg cga aga aaa gca cgt gcc aag 576
 Ala Lys Gln Tyr Glu Gly Ile Leu Arg Arg Arg Lys Ala Arg Ala Lys
 180 185 190

 gca gag cta gag agg aaa gtc atc cgg gac aga aag cca tat ctt cac 624
 Ala Glu Leu Glu Arg Lys Val Ile Arg Asp Arg Arg Lys Pro Tyr Leu His
 195 200 205

 gaa tca aqa cac aag cat gca atg aga agg gca cga gcg agt gga ggc 672
 Ala Lys Gln Tyr Glu Gly Ile Leu Arg Arg Arg Lys Ala Arg Ala Lys

Glu Ser Arg His Lys His Ala Met Arg Arg Ala Arg Ala Ser Gly Gly			
210	215	220	
cgg ttt gcg aag aaa agt gag gta gaa gcg gga gag gat gca gga ggg			720
Arg Phe Ala Lys Lys Ser Glu Val Glu Ala Gly Glu Asp Ala Gly Gly			
225	230	235	240
aga gac aga gaa agg ggt tca gca acc aac tca tca ggc tct gaa caa			768
Arg Asp Arg Glu Arg Gly Ser Ala Thr Asn Ser Ser Gly Ser Glu Gln			
245	250	255	
gtt gag aca gac tct aat gag acc ctg aat tct tct ggt gca cca taa			816
Val Glu Thr Asp Ser Asn Glu Thr Leu Asn Ser Ser Gly Ala Pro			
260	265	270	
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<210> 88			
<211> 271			
<212> PRT			
<213> Arabidopsis thaliana			
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<400> 88			
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His Ala Val Gln Gln Pro Met Met Tyr Ala Glu Pro Trp Trp Lys Asn			
20	25	30	
Asn Ser Phe Gly Val Val Pro Gln Ala Arg Pro Ser Gly Ile Pro Ser			
35	40	45	
Asn Ser Ser Ser Leu Asp Cys Pro Asn Gly Ser Glu Ser Asn Asp Val			
50	55	60	
His Ser Ala Ser Glu Asp Gly Ala Leu Asn Gly Glu Asn Asp Gly Thr			
65	70	75	80
Trp Lys Asp Ser Gln Ala Ala Thr Ser Ser Arg Ser Asp Asn His Gly			
85	90	95	
Met Glu Gly Asn Asp Pro Ala Leu Ser Ile Arg Asn Met His Asp Gln			
100	105	110	
Pro Leu Val Gln Pro Pro Glu Leu Val Gly His Tyr Ile Ala Cys Val			
115	120	125	

Pro Asn Pro Tyr Gln Asp Pro Tyr Tyr Gly Gly Leu Met Gly Ala Tyr
 130 135 140

Gly His Gln Gln Leu Gly Phe Arg Pro Tyr Leu Gly Met Pro Arg Glu
 145 150 155 160

Arg Thr Ala Leu Pro Leu Asp Met Ala Gln Glu Pro Val Tyr Val Asn
 165 170 175

Ala Lys Gln Tyr Glu Gly Ile Leu Arg Arg Arg Lys Ala Arg Ala Lys
 180 185 190

Ala Glu Leu Glu Arg Lys Val Ile Arg Asp Arg Lys Pro Tyr Leu His
 195 200 205

Glu Ser Arg His Lys His Ala Met Arg Arg Ala Arg Ala Ser Gly Gly
 210 215 220

Arg Phe Ala Lys Lys Ser Glu Val Glu Ala Gly Glu Asp Ala Gly Gly
 225 230 235 240

Arg Asp Arg Glu Arg Gly Ser Ala Thr Asn Ser Ser Gly Ser Glu Gln
 245 250 255

Val Glu Thr Asp Ser Asn Glu Thr Leu Asn Ser Ser Gly Ala Pro
 260 265 270

<210> 89

<211> 990

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (1) .. (990)

<223> 71067

<400> 89
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 Met Ser Arg Arg Val Glu Tyr Thr Leu Ala Pro Pro Gln Arg Asn Glu
 1 5 10 15

tct gac ggt ttt gat tat ccc gac ggt atc cca ata tca tac aat ctt	96
Ser Asp Gly Phe Asp Tyr Pro Asp Gly Ile Pro Ile Ser Tyr Asn Leu	
20 25 30	
cat agg ctt cgt cac ttt gag tgt gaa ggc agt tat ccc aag tat cct	144
His Arg Leu Arg His Phe Glu Cys Glu Gly Ser Tyr Pro Lys Tyr Pro	
35 40 45	
tat ggt tct ttg gtc aag ttt tat gca atg gtg gga ctt cat cgt tac	192
Tyr Gly Ser Leu Val Lys Phe Tyr Ala Met Val Gly Leu His Arg Tyr	
50 55 60	
aat gtg ttg gag ggg aaa aat ttg cag ctc gat acc cta aag agt ttc	240
Asn Val Leu Glu Gly Lys Asn Leu Gln Leu Asp Thr Leu Lys Ser Phe	
65 70 75 80	
aac atg aga atc aat tgt ggt gct tct tac tac att act ttg gct	288
Asn Met Arg Ile Asn Cys Gly Ala Ser Ser Tyr Tyr Ile Thr Leu Ala	
85 90 95	
gca cgc gtt cca gat agc ggt ttg aag cag atc ttt cag gtt cta gtt	336
Ala Arg Val Pro Asp Ser Gly Leu Lys Gln Ile Phe Gln Val Leu Val	
100 105 110	
cat gaa gag cgt ctt ggc agt tta gac atg aca tgt act atc gct aga	384
His Glu Glu Arg Leu Gly Ser Leu Asp Met Thr Cys Thr Ile Ala Arg	
115 120 125	
cct cga gtg act acc aat gtg cct ttt cta cgt ccg cac agc gaa tca	432
Pro Arg Val Thr Thr Asn Val Pro Phe Leu Arg Pro His Ser Glu Ser	
130 135 140	
gag tat gat tat atg gac aat gat gaa ttg cct gac tgg cct tca gag	480
Glu Tyr Asp Tyr Met Asp Asn Asp Glu Leu Pro Asp Trp Pro Ser Glu	
145 150 155 160	
att gct ttc gat gat aca aaa cgg ttt cat ctg gtg aag gaa tca gag	528
Ile Ala Phe Asp Asp Thr Lys Arg Phe His Leu Val Lys Glu Ser Glu	
165 170 175	
ttg cga gac aat gat tgg att cga ctc tat ttg gaa ctt aca ctt gtt	576
Leu Arg Asp Asn Asp Trp Ile Arg Leu Tyr Leu Glu Leu Thr Leu Val	
180 185 190	
gct cac gat agg ttt ctt aca gtt cac tat ctc tcc cag ttg gag att	624
Ala His Asp Arg Phe Leu Thr Val His Tyr Leu Ser Gln Leu Glu Ile	
195 200 205	
gtg aaa gtt gcg att gaa gaa gtg gag caa ccg aat gcg agt ctc aac	672
Val Lys Val Ala Ile Glu Glu Val Glu Gln Pro Asn Ala Ser Leu Asn	
210 215 220	
acc aaa act aca ttt gtc tac ata act tat aag gac ttg gca aag gct	720
Thr Lys Thr Phe Val Tyr Ile Thr Tyr Lys Asp Leu Ala Lys Ala	
225 230 235 240	
cag att ggt gag ccg gtt gat cgc aaa gct att gtt aga aaa atc atc	768
Gln Ile Gly Glu Pro Val Asp Arg Lys Ala Ile Val Arg Lys Ile Ile	
245 250 255	

aat gag act acg gga ctc ttg aga ctc cgg ggt gat tat tgg agt gga	816
Asn Glu Thr Thr Gly Leu Leu Arg Leu Arg Gly Asp Tyr Trp Ser Gly	
260 265 270	
gaa aga agt gtg atc act ccg gag gag gaa tat atg ctt ctc cat ggc	864
Glu Arg Ser Val Ile Thr Pro Glu Glu Glu Tyr Met Leu Leu His Gly	
275 280 285	
gga gaa aaa gtt cga aac aat gag cag cgt tct aaa aaa ctt aag cgt	912
Gly Glu Lys Val Arg Asn Asn Glu Gln Arg Ser Lys Lys Leu Lys Arg	
290 295 300	
cgt gta ggt gtt cat agg cta tgg cga tgg tgg tac cag gct tac aaa	960
Arg Val Gly Val His Arg Leu Trp Arg Trp Trp Tyr Gln Ala Tyr Lys	
305 310 315 320	
aac cgt ggc ctc cgc tcg tcg tct tat taa	990
Asn Arg Gly Leu Arg Ser Ser Ser Tyr	
325	

<210> 90

<211> 329

<212> PRT

<213> *Arabidopsis thaliana*

<400> 90

Met Ser Arg Arg Val Glu Tyr Thr Leu Ala Pro Pro Gln Arg Asn Glu	
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Ser Asp Gly Phe Asp Tyr Pro Asp Gly Ile Pro Ile Ser Tyr Asn Leu	
20 25 30	

His Arg Leu Arg His Phe Glu Cys Glu Gly Ser Tyr Pro Lys Tyr Pro	
35 40 45	

Tyr Gly Ser Leu Val Lys Phe Tyr Ala Met Val Gly Leu His Arg Tyr	
50 55 60	

Asn Val Leu Glu Gly Lys Asn Leu Gln Leu Asp Thr Leu Lys Ser Phe	
65 70 75 80	

Asn Met Arg Ile Asn Cys Gly Ala Ser Ser Tyr Tyr Ile Thr Leu Ala	
85 90 95	

Ala Arg Val Pro Asp Ser Gly Leu Lys Gln Ile Phe Gln Val Leu Val	
100 105 110	

His Glu Glu Arg Leu Gly Ser Leu Asp Met Thr Cys Thr Ile Ala Arg
115 120 125

Pro Arg Val Thr Thr Asn Val Pro Phe Leu Arg Pro His Ser Glu Ser
130 135 140

Glu Tyr Asp Tyr Met Asp Asn Asp Glu Leu Pro Asp Trp Pro Ser Glu
145 150 155 160

Ile Ala Phe Asp Asp Thr Lys Arg Phe His Leu Val Lys Glu Ser Glu
165 170 175

Leu Arg Asp Asn Asp Trp Ile Arg Leu Tyr Leu Glu Leu Thr Leu Val
180 185 190

Ala His Asp Arg Phe Leu Thr Val His Tyr Leu Ser Gln Leu Glu Ile
195 200 205

Val Lys Val Ala Ile Glu Glu Val Glu Gln Pro Asn Ala Ser Leu Asn
210 215 220

Thr Lys Thr Thr Phe Val Tyr Ile Thr Tyr Lys Asp Leu Ala Lys Ala
225 230 235 240

Gln Ile Gly Glu Pro Val Asp Arg Lys Ala Ile Val Arg Lys Ile Ile
245 250 255

Asn Glu Thr Thr Gly Leu Leu Arg Leu Arg Gly Asp Tyr Trp Ser Gly
260 265 270

Glu Arg Ser Val Ile Thr Pro Glu Glu Glu Tyr Met Leu Leu His Gly
275 280 285

Gly Glu Lys Val Arg Asn Asn Glu Gln Arg Ser Lys Lys Leu Lys Arg
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 Ser Ser Arg Phe Gly Ser Leu Tyr Val Gly Asp Leu Ser Pro Asp Val
 20 25 30

 acg gag aaa gat ctc att gat aag ttc tct ttg aat gtt ccg gta gtg 144
 Thr Glu Lys Asp Leu Ile Asp Lys Phe Ser Leu Asn Val Pro Val Val
 35 40 45

 tcc gtt cat ctt tgc cgt aac tct gtc acc gga aaa tcc atg tgt tac 192
 Ser Val His Leu Cys Arg Asn Ser Val Thr Gly Lys Ser Met Cys Tyr
 50 55 60

 gct tac atc aac ttc gat tca cct ttc agc gca tcg aat gct atg act 240
 Ala Tyr Ile Asn Phe Asp Ser Pro Phe Ser Ala Ser Asn Ala Met Thr
 65 70 75 80

 cgc tta aac cat agt gat ttg aag gga aag gct atg cga ata atg tgg 288
 Arg Leu Asn His Ser Asp Leu Lys Gly Lys Ala Met Arg Ile Met Trp
 85 90 95

 tct cag agg gat ctt gcg tac cgt cgt act cgt act ggt ttt gca 336
 Ser Gln Arg Asp Leu Ala Tyr Arg Arg Thr Arg Thr Gly Phe Ala
 100 105 110

 aat cta tac gta aag aat ctg gat agc tcg att act agc agt tgc tta 384
 Asn Leu Tyr Val Lys Asn Leu Asp Ser Ser Ile Thr Ser Ser Cys Leu
 115 120 125

 gag cga atg ttt tgc ccc ttt ggt tcc ata ctt tct tgc aaa gtc gtt 432
 Glu Arg Met Phe Cys Pro Phe Gly Ser Ile Leu Ser Cys Lys Val Val
 130 135 140

 gaa gag aat ggc caa agt aaa ggt ttt ggc ttt gtt cag ttt gat aca 480
 Glu Glu Asn Gly Gln Ser Lys Gly Phe Gly Phe Val Gln Phe Asp Thr
 145 150 155 160

 qaq caa tct gct gta tct gct cgt tct gct ctc cac ggc tct atg gtt 528

Glu	Gln	Ser	Ala	Val	Ser	Ala	Arg	Ser	Ala	Leu	His	Gly	Ser	Met	Val	
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tat ggc aag aaa ctg ttt gtt gcc aag ttc atc aac aag gat gaa aga															576	
Tyr	Gly	Lys	Lys	Leu	Phe	Val	Ala	Lys	Phe	Ile	Asn	Lys	Asp	Glu	Arg	
180																190
gca gct atg gca gga aat caa gac tct aca aac gtt tat gtg aag aat															624	
Ala	Ala	Met	Ala	Gly	Asn	Gln	Asp	Ser	Thr	Asn	Val	Tyr	Val	Lys	Asn	
195																205
ctg atc gaa act gtt aca gat gat tgt cta cat aca ctg ttt tct caa															672	
Leu	Ile	Glu	Thr	Val	Thr	Asp	Asp	Cys	Leu	His	Thr	Leu	Phe	Ser	Gln	
210																220
tat gga act gtc tct agt gtt gtg gtt atg agg gat ggt atg gga aga															720	
Tyr	Gly	Thr	Val	Ser	Ser	Val	Val	Met	Arg	Asp	Gly	Met	Gly	Arg		
225																240
tct aga ggt ttc gga ttt gtt aac ttc tgc aat cca gaa aat gct aag															768	
Ser	Arg	Gly	Phe	Gly	Phe	Val	Asn	Phe	Cys	Asn	Pro	Glu	Asn	Ala	Lys	
245																255
aaa gct atg gaa tct ctc tgt gga cta caa ctt gga tcg aag aaa ttg															816	
Lys	Ala	Met	Glu	Ser	Ieu	Cys	Gly	Leu	Gln	Leu	Gly	Ser	Lys	Lys	Leu	
260																270
ttt gtt ggt aag gca ctc aag aaa gat gaa agg agg gag atg ctg aaa															864	
Phe	Val	Gly	Lys	Ala	Ieu	Lys	Asp	Glu	Arg	Arg	Glu	Met	Leu	Lys		
275																285
cag aaa ttc agt gac aac ttt att gca aag cct aac atg aga tgg tcc															912	
Gln	Lys	Phe	Ser	Asp	Asn	Phe	Ile	Ala	Lys	Pro	Asn	Met	Arg	Trp	Ser	
290																300
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Asn	Leu	Tyr	Val	Lys	Asn	Ieu	Ser	Glu	Ser	Met	Asn	Glu	Thr	Arg	Leu	
305																320
cga gaa atc ttt gga tgc tat ggg caa ata gtt tca gct aaa gtg atg															1008	
Arg	Glu	Ile	Phe	Gly	Cys	Tyr	Gly	Gln	Ile	Val	Ser	Ala	Lys	Val	Met	
325																335
tgt cat gag aat ggc aga agt aaa gga ttc ggc ttt gtg tgc ttc tct															1056	
Cys	His	Glu	Asn	Gly	Arg	Ser	Lys	Gly	Phe	Gly	Phe	Val	Cys	Phe	Ser	
340																350
aac tgt gaa gag tcc aaa cag gct aaa aga tat ctc aat ggg ttc tta															1104	
Asn	Cys	Glu	Ser	Lys	Gln	Ala	Lys	Arg	Tyr	Leu	Asn	Gly	Phe	Leu		
355																365
gtt gat gga aag cca ata gtt gtt cga gtt gca gag cgc aaa gag gat															1152	
Val	Asp	Gly	Lys	Pro	Ile	Val	Val	Arg	Val	Ala	Glu	Arg	Lys	Glu	Asp	
370																380
cga atc aag agg ttg cag caa tat ttt cag gca cag cca cgc cag tac															1200	
Arg	Ile	Lys	Arg	Leu	Gln	Gln	Tyr	Phe	Gln	Ala	Gln	Pro	Arg	Gln	Tyr	
385																400
acg caa gct cct tct gcc cct tca cca gct cag cca gtc ctc tca tat															1248	

Thr Gln Ala Pro Ser Ala Pro Ser Pro Ala Gln Pro Val Leu Ser Tyr			
405	410	415	
gtg tcc agc tca tat ggt tgc ttt cag cca ttc cag gtc ggg aca tct			1296
Val Ser Ser Ser Tyr Gly Cys Phe Gln Pro Phe Gln Val Gly Thr Ser			
420	425	430	
tat tac tat atg ggc aat cag gtg cca caa atg tcc ggt cac caa aac			1344
Tyr Tyr Tyr Met Gly Asn Gln Val Pro Gln Met Ser Gly His Gln Asn			
435	440	445	
atc acc acc tac gtt cca gct ggg aaa gtg cct ctc aag gag aga aga			1392
Ile Thr Thr Tyr Val Pro Ala Gly Lys Val Pro Leu Lys Glu Arg Arg			
450	455	460	
tca atg cat ctg gtc tac aaa cat ccg gct tat ccc gtt gcc aag agg			1440
Ser Met His Leu Val Tyr Lys His Pro Ala Tyr Pro Val Ala Lys Arg			
465	470	475	480
ggt gct aaa cag aca ctg gtt ttt aag ggt gag gtt aac aga aat tta			1488
Gly Ala Lys Gln Thr Ieu Val Phe Lys Gly Glu Val Asn Arg Asn Leu			
485	490	495	
gag gct gca aca tgc tcc aaa gca aca aca tct gag gag aac cgt aaa			1536
Glu Ala Ala Thr Cys Ser Lys Ala Thr Thr Ser Glu Glu Asn Arg Lys			
500	505	510	
gaa gaa cga aga ttg act ttg tca gga aag ttg tca cca gaa gtg aag			1584
Glu Glu Arg Arg Leu Thr Leu Ser Gly Lys Leu Ser Pro Glu Val Lys			
515	520	525	
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Thr Glu Lys Asp Leu Ile Asp Lys Phe Ser Leu Asn Val Pro Val Val			
35	40	45	

Ser Val His Leu Cys Arg Asn Ser Val Thr Gly Lys Ser Met Cys Tyr
50 55 60

Ala Tyr Ile Asn Phe Asp Ser Pro Phe Ser Ala Ser Asn Ala Met Thr
65 70 75 80

Arg Leu Asn His Ser Asp Leu Lys Gly Lys Ala Met Arg Ile Met Trp
85 90 95

Ser Gln Arg Asp Leu Ala Tyr Arg Arg Arg Thr Arg Thr Gly Phe Ala
100 105 110

Asn Leu Tyr Val Lys Asn Leu Asp Ser Ser Ile Thr Ser Ser Cys Leu
115 120 125

Glu Arg Met Phe Cys Pro Phe Gly Ser Ile Leu Ser Cys Lys Val Val
130 135 140

Glu Glu Asn Gly Gln Ser Lys Gly Phe Gly Phe Val Gln Phe Asp Thr
145 150 155 160

Glu Gln Ser Ala Val Ser Ala Arg Ser Ala Leu His Gly Ser Met Val
165 170 175

Tyr Gly Lys Leu Phe Val Ala Lys Phe Ile Asn Lys Asp Glu Arg
180 185 190

Ala Ala Met Ala Gly Asn Gln Asp Ser Thr Asn Val Tyr Val Lys Asn
195 200 205

Leu Ile Glu Thr Val Thr Asp Asp Cys Leu His Thr Leu Phe Ser Gln
210 215 220

Tyr Gly Thr Val Ser Ser Val Val Met Arg Asp Gly Met Gly Arg
225 230 235 240

Ser Arg Gly Phe Gly Phe Val Asn Phe Cys Asn Pro Glu Asn Ala Lys
245 250 255

Lys Ala Met Glu Ser Leu Cys Gly Leu Gln Leu Gly Ser Lys Lys Leu
260 265 270

Phe Val Gly Lys Ala Leu Lys Lys Asp Glu Arg Arg Glu Met Leu Lys
275 280 285

Gln Lys Phe Ser Asp Asn Phe Ile Ala Lys Pro Asn Met Arg Trp Ser
290 295 300

Asn Leu Tyr Val Lys Asn Leu Ser Glu Ser Met Asn Glu Thr Arg Leu
305 310 315 320

Arg Glu Ile Phe Gly Cys Tyr Gly Gln Ile Val Ser Ala Lys Val Met
325 330 335

Cys His Glu Asn Gly Arg Ser Lys Gly Phe Gly Phe Val Cys Phe Ser
340 345 350

Asn Cys Glu Glu Ser Lys Gln Ala Lys Arg Tyr Leu Asn Gly Phe Leu
355 360 365

Val Asp Gly Lys Pro Ile Val Val Arg Val Ala Glu Arg Lys Glu Asp
370 375 380

Arg Ile Lys Arg Leu Gln Gln Tyr Phe Gln Ala Gln Pro Arg Gln Tyr
385 390 395 400

Thr Gln Ala Pro Ser Ala Pro Ser Pro Ala Gln Pro Val Leu Ser Tyr
405 410 415

Val Ser Ser Ser Tyr Gly Cys Phe Gln Pro Phe Gln Val Gly Thr Ser
420 425 430

Tyr Tyr Tyr Met Gly Asn Gln Val Pro Gln Met Ser Gly His Gln Asn
435 440 445

Ile Thr Thr Tyr Val Pro Ala Gly Lys Val Pro Leu Lys Glu Arg Arg
450 455 460

Ser Met His Leu Val Tyr Lys His Pro Ala Tyr Pro Val Ala Lys Arg
465 470 475 480

Gly Ala Lys Gln Thr Leu Val Phe Lys Gly Glu Val Asn Arg Asn Leu
485 490 495

Glu Ala Ala Thr Cys Ser Lys Ala Thr Thr Ser Glu Glu Asn Arg Lys
500 505 510

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gaa gaa caa cac tat tct tta tca aga ctc tcc gtt tgt tcc aac tac		96
Glu Glu Gln His Tyr Ser Leu Ser Arg Leu Ser Val Cys Ser Asn Tyr		
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gac ggc gat gaa gcc gac ggt gag tct tct gct tcc gac gag aaa cgt		144
Asp Gly Asp Glu Ala Asp Gly Glu Ser Ser Ala Ser Asp Glu Lys Arg		
35 40 45		
gtt gtc cac ggc gga gga gag aaa tcc atg gag gag ota aat ttt tca		192
Val Val His Gly Gly Glu Lys Ser Met Glu Glu Leu Asn Phe Ser		
50 55 60		
gat tct gat aaa gaa tca acc ggt tgt caa tct ctc ccg gcg aca cct		240
Asp Ser Asp Lys Glu Ser Thr Gly Cys Gln Ser Leu Pro Ala Thr Pro		
65 70 75 80		
ccg aga cgg aga cgg cgg aga ggc ggt gga gga gga gga tat tta gcg		288
Pro Arg Arg Arg Arg Arg Gly Gly Gly Gly Tyr Leu Ala		
85 90 95		
gtg agt tct ccg gtt tcc ggc gat aaa gct tac gct agc gag aac gaa		336
Val Ser Ser Pro Val Ser Gly Asp Lys Ala Tyr Ala Ser Glu Asn Glu		
100 105 110		
gta caa aag acg aat aac aat cag agg aga agg agg aga ttg aaa ccg		384
Val Gln Lys Thr Asn Asn Asn Gln Arg Arg Arg Arg Leu Lys Pro		
115 120 125		
gag tgt cca ccg tgg gtt gat agt atg cgg agg agc tac gtc gga gat		432
Glu Cys Pro Pro Trp Val Asp Ser Met Arg Arg Arg Tyr Val Gly Asp		
130 135 140		

gaa cag agt agt cac ggt ggt tac gga gga gga gtg gtg gtt gtt acg	145	150	155	160	480
Glu Gln Ser Ser His Gly Gly Tyr Gly Gly Val Val Val Val Thr					
agg cct ata gga gga gga agg cca ttg tgt atg gat tta gaa gaa gtc	165	170	175		528
Arg Pro Ile Gly Gly Arg Pro Leu Cys Met Asp Leu Glu Glu Val					
aaa gct tgt aaa gat ttg ggg ttt gag ctt gaa ccg ggt cgg gtt tcg	180	185	190		576
Lys Ala Cys Lys Asp Leu Gly Phe Glu Leu Glu Pro Gly Arg Val Ser					
tat tcc ggg tca acg gtg gat act agt agt ggc ggc aat tct cct atc	195	200	205		624
Tyr Ser Gly Ser Thr Val Asp Thr Ser Ser Gly Gly Asn Ser Pro Ile					
tct tct aac cac cgt att tcg agt ccc ggt tag	210	215			657
Ser Ser Asn His Arg Ile Ser Ser Pro Gly					
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1	5	10	15		
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20	25	30			
Asp Gly Asp Glu Ala Asp Gly Glu Ser Ser Ala Ser Asp Glu Lys Arg	35	40	45		
35	40	45			
Val Val His Gly Gly Glu Lys Ser Met Glu Glu Leu Asn Phe Ser	50	55	60		
50	55	60			
Asp Ser Asp Lys Glu Ser Thr Gly Cys Gln Ser Leu Pro Ala Thr Pro	65	70	75	80	
65	70	75	80		
Pro Arg Arg Arg Arg Arg Gly Gly Gly Gly Gly Tyr Leu Ala	85	90	95		
85	90	95			
Val Ser Ser Pro Val Ser Gly Asp Lys Ala Tyr Ala Ser Glu Asn Glu	100	105	110		
100	105	110			

Val Gln Lys Thr Asn Asn Asn Gln Arg Arg Arg Arg Arg Leu Lys Pro
 115 120 125

Glu Cys Pro Pro Trp Val Asp Ser Met Arg Arg Ser Tyr Val Gly Asp
 130 135 140

Glu Gln Ser Ser His Gly Gly Tyr Gly Gly Val Val Val Val Thr
 145 150 155 160

Arg Pro Ile Gly Gly Arg Pro Leu Cys Met Asp Leu Glu Glu Val
 165 170 175

Lys Ala Cys Lys Asp Leu Gly Phe Glu Leu Glu Pro Gly Arg Val Ser
 180 185 190

Tyr Ser Gly Ser Thr Val Asp Thr Ser Ser Gly Gly Asn Ser Pro Ile
 195 200 205

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gtc tac aaa aat gct att ttc atg tgc gag cgt ctc tgc gct gag ttt 96
 Val Tyr Lys Asn Ala Ile Phe Met Cys Glu Arg Leu Cys Ala Glu Phe
 20 25 30

cct tct gag gtt aat ttg cag cta tta gcc acc agc tac ctg cag aat 144

Pro Ser Glu Val Asn Leu Gln Leu Leu Ala Thr Ser Tyr Leu Gln Asn			
35	40	45	
aat caa gct tac agt gca tat cat ctg cta aag gga aca caa atg gct			192
Asn Gln Ala Tyr Ser Ala Tyr His Leu Leu Lys Gly Thr Gln Met Ala			
50	55	60	
cag tcc cga tac ttg ttc gca tta tca tgc ttc cag atg gac ctt ctc			240
Gln Ser Arg Tyr Leu Phe Ala Leu Ser Cys Phe Gln Met Asp Leu Leu			
65	70	75	80
aat gaa gct gaa tct gca ctc tgc cct gtt aat gaa cct ggt gcg gag			288
Asn Glu Ala Glu Ser Ala Leu Cys Pro Val Asn Glu Pro Gly Ala Glu			
85	90	95	
atc cca aat ggt gca gca ggc cat tac ctt ctt gga ctt att tac aag			336
Ile Pro Asn Gly Ala Ala Gly His Tyr Leu Leu Gly Leu Ile Tyr Lys			
100	105	110	
aag aat gct gct caa caa ttt aaa cag tcc ttg aca ata gac cct cta			384
Lys Asn Ala Ala Gln Gln Phe Lys Gln Ser Leu Thr Ile Asp Pro Leu			
115	120	125	
ctt tgg gct gca tat gag gaa tta tgt ata tta ggt gct gct gag gaa			432
Leu Trp Ala Ala Tyr Glu Glu Leu Cys Ile Leu Gly Ala Ala Glu Glu			
130	135	140	
gca act gca gtt ttt ggt gaa aca gct gct ctc tcc att caa aag cag			480
Ala Thr Ala Val Phe Gly Glu Thr Ala Ala Leu Ser Ile Gln Lys Gln			
145	150	155	160
tat atg caa caa ctg tca act tcc ctc ggc tta aac act tac aac gag			528
Tyr Met Gln Gln Leu Ser Thr Ser Leu Gly Leu Asn Thr Tyr Asn Glu			
165	170	175	
gaa cgt aat tca act tct act aaa aac acg agt tct gaa gat tat agt			576
Glu Arg Asn Ser Thr Ser Thr Lys Asn Thr Ser Ser Glu Asp Tyr Ser			
180	185	190	
cca agg cag tct aaa cac aca caa agc cat ggc ctt aaa gat atc tcc			624
Pro Arg Gln Ser Lys His Thr Gln Ser His Gly Leu Lys Asp Ile Ser			
195	200	205	
gga aat ttc cat tct cat gga gtt aat gga ggt gtt tcg aac atg tca			672
Gly Asn Phe His Ser His Gly Val Asn Gly Gly Val Ser Asn Met Ser			
210	215	220	
ttc tat aat acg cct tcg cca gtg gct gca cag cta tcc ggt ata gct			720
Phe Tyr Asn Thr Pro Ser Pro Val Ala Ala Gln Leu Ser Gly Ile Ala			
225	230	235	240
cca cca cca ctt ttc cgg aat ttt cag cca gct gtt gca aac cca aac			768
Pro Pro Pro Leu Phe Arg Asn Phe Gln Pro Ala Val Ala Asn Pro Asn			
245	250	255	
tcc ctt att act gac agt tct cca aag tcc act gtt aac tct act ctt			816
Ser Leu Ile Thr Asp Ser Ser Pro Lys Ser Thr Val Asn Ser Thr Leu			
260	265	270	
caa gca cct aga aga aag ttt gta gat gaa gga aag tta cgt aag att			864

Gln Ala Pro Arg Arg Lys Phe Val Asp Glu Gly Lys Leu Arg Lys Ile			
275	280	285	
tct ggc aga cta ttt tct gat tct ggt cca cga cgg agt tca aga ctg			912
Ser Gly Arg Leu Phe Ser Asp Ser Gly Pro Arg Arg Ser Ser Arg Leu			
290	295	300	
tct gct gat tca ggg gca aac att aat tca agt gtt gca aca gta agc			960
Ser Ala Asp Ser Gly Ala Asn Ile Asn Ser Ser Val Ala Thr Val Ser			
305	310	315	320
gga aat gtg aac aac gct tcc aag tat ttg gga ggt tct aaa ttg agt			1008
Gly Asn Val Asn Asn Ala Ser Lys Tyr Leu Gly Ser Lys Leu Ser			
325	330	335	
tct ttg gca ctt cgt tct gta aca ctt cgg aag gga cac tcc tgg gca			1056
Ser Leu Ala Leu Arg Ser Val Thr Leu Arg Lys Gly His Ser Trp Ala			
340	345	350	
aat gaa aac atg gat gaa ggg gtc cgt ggg gaa cct ttt gat gat tca			1104
Asn Glu Asn Met Asp Glu Gly Val Arg Gly Glu Pro Phe Asp Asp Ser			
355	360	365	
agg cct aat act gcc tca acg act ggt tct atg gct tcc aat gat caa			1152
Arg Pro Asn Thr Ala Ser Thr Thr Gly Ser Met Ala Ser Asn Asp Gln			
370	375	380	
gaa gac gaa aca atg tcg att ggt ggc ata gca atg agt tct caa aca			1200
Glu Asp Glu Thr Met Ser Ile Gly Gly Ile Ala Met Ser Ser Gln Thr			
385	390	395	400
atc aca att ggt gtt tcg gaa att tta aac ctc ctt agg aca ctc gga			1248
Ile Thr Ile Gly Val Ser Glu Ile Leu Asn Leu Leu Arg Thr Leu Gly			
405	410	415	
gaa ggg tgt aga ctt tca tac atg tac agg tgt cag gag gca ctg gat			1296
Glu Gly Cys Arg Leu Ser Tyr Met Tyr Arg Cys Gln Glu Ala Leu Asp			
420	425	430	
acg tat atg aaa ctt cca cat aag cat tat aat aca gga tgg gtt ctt			1344
Thr Tyr Met Lys Leu Pro His Lys His Tyr Asn Thr Gly Trp Val Leu			
435	440	445	
tcc cag gtc ggg aaa gca tac ttt gaa cta att gac tat tta gag gct			1392
Ser Gln Val Gly Lys Ala Tyr Phe Glu Leu Ile Asp Tyr Leu Glu Ala			
450	455	460	
gaa aag gca ttc cgt ctt gcc cgt ctg gct tct cct tat tgc tta gaa			1440
Glu Lys Ala Phe Arg Leu Ala Arg Leu Ala Ser Pro Tyr Cys Leu Glu			
465	470	475	480
gga atg gat ata tac tct acg gtc ctc tat cat ttg aag gaa gac atg			1488
Gly Met Asp Ile Tyr Ser Thr Val Leu Tyr His Leu Lys Glu Asp Met			
485	490	495	
aag ctg agt tac ttg gct cag gaa cta ata tca acc gat cgc tta gct			1536
Lys Leu Ser Tyr Leu Ala Gln Glu Leu Ile Ser Thr Asp Arg Leu Ala			
500	505	510	
cct caa tct tgg tgt gct atg gga aat tgc tat agc ttg caa aag gac			1584

Pro Gln Ser Trp Cys Ala Met Gly Asn Cys Tyr Ser Leu Gln Lys Asp			
515	520	525	
cat gag acc gca ctg aag aat ttc cta cga gct gtt caa ctg aat cca			1632
His Glu Thr Ala Leu Lys Asn Phe Leu Arg Ala Val Gln Leu Asn Pro			
530	535	540	
aga ttt gca tat gca cat acc tta tgt ggc cac gaa tac aca act ctt			1680
Arg Phe Ala Tyr Ala His Thr Leu Cys Gly His Glu Tyr Thr Leu			
545	550	555	560
gag gat ttt gag aac gga atg aaa agt tac caa aac gca ctt cgt gta			1728
Glu Asp Phe Glu Asn Gly Met Lys Ser Tyr Gln Asn Ala Leu Arg Val			
565	570	575	
gat aca aga cac tac aac gca tgg tac ggg ctt gga atg ata tat cta			1776
Asp Thr Arg His Tyr Asn Ala Trp Tyr Gly Leu Gly Met Ile Tyr Leu			
580	585	590	
cgc caa gag aag tta gag ttc tca gag cat cac ttc aga atg gct ttc			1824
Arg Gln Glu Lys Leu Glu Phe Ser Glu His His Phe Arg Met Ala Phe			
595	600	605	
cta ata aac cog agt tcc tct gtt ata atg tct tat tta ggg aca tct			1872
Leu Ile Asn Pro Ser Ser Val Ile Met Ser Tyr Leu Gly Thr Ser			
610	615	620	
ttg cat gcc ttg aag aga agt gag gaa gca cta gag ata atg gag caa			1920
Leu His Ala Leu Lys Arg Ser Glu Glu Ala Leu Glu Ile Met Glu Gln			
625	630	635	640
gcc ata gta gca gat aga aaa aac cct ctt cca atg tac cag aaa gct			1968
Ala Ile Val Ala Asp Arg Lys Asn Pro Leu Pro Met Tyr Gln Lys Ala			
645	650	655	
aac ata ctt gtc tgc tta gaa aga tta gat gaa gct cta gaa gtt ctt			2016
Asn Ile Leu Val Cys Leu Glu Arg Leu Asp Glu Ala Leu Glu Val Leu			
660	665	670	
gag gag ctc aaa gag tat gcg cct tca gag agc agc gtt tac gct tta			2064
Glu Glu Leu Lys Glu Tyr Ala Pro Ser Glu Ser Ser Val Tyr Ala Leu			
675	680	685	
atg ggc agg atc tat aag cgg cga aac atg cac gat aaa gcc atg ctt			2112
Met Gly Arg Ile Tyr Lys Arg Arg Asn Met His Asp Lys Ala Met Leu			
690	695	700	
cat ttc ggt cta gct tta gat atg aaa ccg cct gca act gac gtt gct			2160
His Phe Gly Leu Ala Leu Asp Met Lys Pro Pro Ala Thr Asp Val Ala			
705	710	715	720
gca ata aag gct gca atg gag aaa ttg cat gtt cca gat gag atc gat			2208
Ala Ile Lys Ala Ala Met Glu Lys Leu His Val Pro Asp Glu Ile Asp			
725	730	735	
gag agc ccg tga			2220
Glu Ser Pro			

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<211> 739

<212> PRT

<213> *Arabidopsis thaliana*

<400> 96

Met Glu Ala Met Leu Val Asp Cys Val Asn Asn Ser Leu Arg His Phe
1 5 10 15

Val Tyr Lys Asn Ala Ile Phe Met Cys Glu Arg Leu Cys Ala Glu Phe
20 25 30

Pro Ser Glu Val Asn Leu Gln Leu Ala Thr Ser Tyr Leu Gln Asn
35 40 45

Asn Gln Ala Tyr Ser Ala Tyr His Leu Leu Lys Gly Thr Gln Met Ala
50 55 60

Gln Ser Arg Tyr Leu Phe Ala Leu Ser Cys Phe Gln Met Asp Leu Leu
65 70 75 80

Asn Glu Ala Glu Ser Ala Leu Cys Pro Val Asn Glu Pro Gly Ala Glu
85 90 95

Ile Pro Asn Gly Ala Ala Gly His Tyr Leu Leu Gly Leu Ile Tyr Lys
100 105 110

Lys Asn Ala Ala Gln Gln Phe Lys Gln Ser Leu Thr Ile Asp Pro Leu
115 120 125

Leu Trp Ala Ala Tyr Glu Glu Leu Cys Ile Leu Gly Ala Ala Glu Glu
130 135 140

Ala Thr Ala Val Phe Gly Glu Thr Ala Ala Leu Ser Ile Gln Lys Gln
145 150 155 160

Tyr Met Gln Gln Leu Ser Thr Ser Leu Gly Leu Asn Thr Tyr Asn Glu
165 170 175

Glu Arg Asn Ser Thr Ser Thr Lys Asn Thr Ser Ser Glu Asp Tyr Ser
180 185 190

Pro Arg Gln Ser Lys His Thr Gln Ser His Gly Leu Lys Asp Ile Ser
195 200 205

Gly Asn Phe His Ser His Gly Val Asn Gly Gly Val Ser Asn Met Ser
210 215 220

Phe Tyr Asn Thr Pro Ser Pro Val Ala Ala Gln Leu Ser Gly Ile Ala
225 230 235 240

Pro Pro Pro Leu Phe Arg Asn Phe Gln Pro Ala Val Ala Asn Pro Asn
245 250 255

Ser Leu Ile Thr Asp Ser Ser Pro Lys Ser Thr Val Asn Ser Thr Leu
260 265 270

Gln Ala Pro Arg Arg Lys Phe Val Asp Glu Gly Lys Leu Arg Lys Ile
275 280 285

Ser Gly Arg Leu Phe Ser Asp Ser Gly Pro Arg Arg Ser Ser Arg Leu
290 295 300

Ser Ala Asp Ser Gly Ala Asn Ile Asn Ser Ser Val Ala Thr Val Ser
305 310 315 320

Gly Asn Val Asn Asn Ala Ser Lys Tyr Leu Gly Gly Ser Lys Leu Ser
325 330 335

Ser Leu Ala Leu Arg Ser Val Thr Leu Arg Lys Gly His Ser Trp Ala
340 345 350

Asn Glu Asn Met Asp Glu Gly Val Arg Gly Glu Pro Phe Asp Asp Ser
355 360 365

Arg Pro Asn Thr Ala Ser Thr Thr Gly Ser Met Ala Ser Asn Asp Gln
370 375 380

Glu Asp Glu Thr Met Ser Ile Gly Gly Ile Ala Met Ser Ser Gln Thr
385 390 395 400

Ile Thr Ile Gly Val Ser Glu Ile Leu Asn Leu Leu Arg Thr Leu Gly
405 410 415

Glu Gly Cys Arg Leu Ser Tyr Met Tyr Arg Cys Gln Glu Ala Leu Asp
420 425 430

Thr Tyr Met Lys Leu Pro His Lys His Tyr Asn Thr Gly Trp Val Leu
435 440 445

Ser Gln Val Gly Lys Ala Tyr Phe Glu Leu Ile Asp Tyr Leu Glu Ala
450 455 460

Glu Lys Ala Phe Arg Leu Ala Arg Leu Ala Ser Pro Tyr Cys Leu Glu
465 470 475 480

Gly Met Asp Ile Tyr Ser Thr Val Leu Tyr His Leu Lys Glu Asp Met
485 490 495

Lys Leu Ser Tyr Leu Ala Gln Glu Leu Ile Ser Thr Asp Arg Leu Ala
500 505 510

Pro Gln Ser Trp Cys Ala Met Gly Asn Cys Tyr Ser Leu Gln Lys Asp
515 520 525

His Glu Thr Ala Leu Lys Asn Phe Leu Arg Ala Val Gln Leu Asn Pro
530 535 540

Arg Phe Ala Tyr Ala His Thr Leu Cys Gly His Glu Tyr Thr Thr Leu
545 550 555 560

Glu Asp Phe Glu Asn Gly Met Lys Ser Tyr Gln Asn Ala Leu Arg Val
565 570 575

Asp Thr Arg His Tyr Asn Ala Trp Tyr Gly Leu Gly Met Ile Tyr Leu
580 585 590

Arg Gln Glu Lys Leu Glu Phe Ser Glu His His Phe Arg Met Ala Phe
595 600 605

Leu Ile Asn Pro Ser Ser Val Ile Met Ser Tyr Leu Gly Thr Ser
610 615 620

Leu His Ala Leu Lys Arg Ser Glu Glu Ala Leu Glu Ile Met Glu Gln
625 630 635 640

Ala Ile Val Ala Asp Arg Lys Asn Pro Leu Pro Met Tyr Gln Lys Ala
645 650 655

Asn Ile Leu Val Cys Leu Glu Arg Leu Asp Glu Ala Leu Glu Val Leu
660 665 670

Glu Glu Leu Lys Glu Tyr Ala Pro Ser Glu Ser Ser Val Tyr Ala Leu
675 680 685

Met Gly Arg Ile Tyr Lys Arg Arg Asn Met His Asp Lys Ala Met Leu
690 695 700

His Phe Gly Leu Ala Leu Asp Met Lys Pro Pro Ala Thr Asp Val Ala
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Ala Ile Lys Ala Ala Met Glu Lys Leu His Val Pro Asp Glu Ile Asp
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Glu Ser Pro

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